

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2004, 02:36:13 ; Search time 1292 Seconds
(without alignments)

11249.628 Million cell updates/sec

Title: US-09-900-448-1

Perfect score: 3186

Sequence: 1 cctgcagctcagcatggctt.....accttttctgtgttctca 3186

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3186	100.0	3186	11	US-09-900-448-1
2	2279.2	71.5	13737	11	Sequence 1, Appli
3	1129.8	35.5	1631	15	Sequence 3, Appli
4	1129.8	35.5	1631	15	Sequence 19, Appli
5	644.8	20.2	861	16	Sequence 19, Appli
6	576.8	18.1	1516	15	Sequence 87, Appli
7	576.8	18.1	1516	15	Sequence 84, Appli
8	427	13.4	488	10	Sequence 39, Appli
9	421	13.2	422	10	Sequence 30828, A
10	417	13.1	492	10	Sequence 8595, Ap
11	374.2	11.7	488	10	Sequence 31395, A
12	345.4	10.8	491	10	Sequence 30754, A
13	313.4	9.8	504	9	Sequence 32820, A
14	298.4	9.4	420	9	Sequence 3165, Ap
					Sequence 10323, A

Sequence 7040, Ap
Sequence 7738, Ap
Sequence 32181, A
Sequence 5368, Ap
Sequence 6846, Ap
Sequence 380, App
Sequence 445, App
Sequence 3702, Ap
Sequence 9378, Ap
Sequence 12935, A
Sequence 1316, A
Sequence 7056, Ap
Sequence 13395, A
Sequence 2026, Ap
Sequence 2507, Ap
Sequence 13402, A
Sequence 7514, A
Sequence 8662, Ap
Sequence 13176, A
Sequence 7320, Ap
Sequence 457, App
Sequence 136, App
Sequence 6107, Ap
Sequence 5619, Ap
Sequence 4209, Ap
Sequence 5320, Ap
Sequence 2556, Ap
Sequence 13635, A
Sequence 7025, Ap
Sequence 1789, Ap
Sequence 9132, Ap

ALIGNMENTS

RESULT 1

US-09-900-448-1
; Sequence 1, Application US/09900448
; Publication No. US2003022048BA1
; GENERAL INFORMATION:
; APPLICANT: CECARDI, Toni et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001272
; CURRENT APPLICATION NUMBER: US/09/900,448
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3186
; TYPE: DNA
; ORGANISM: Human
US-09-900-448-1

Query Match Similarity 100.0%; Score 3186; DB 11; Length 3186;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCTGCAGCTCAGCATGGCTAGGCTACTGGAGCACCCTGGTGCACCTGGGTTGTGGAGCC 60
DB 1 CTCTGCAGCTCAGCATGGCTAGGCTACTGGAGCACCCTGGTGCACCTGGGTTGTGGAGCC 60
QY 61 TATGCTGCTCTGCGCATTCGCCACCCCTCTTCTCGACTAGTCCGCAATGTTG 120
DB 61 TATGCTGCTCTGCGCATTCGCCACCCCTCTTCTCGACTAGTCCGCAATGTTG 120
QY 121 CTGAAGCGGAGACCAACCCAGACCCAGACCTGCTGACCTGCTCAGATGGCTGGAGCT 180
DB 121 CTGAAGCGGAGACCAACCCAGACCCAGACCTGCTGACCTGCTCAGATGGCTGGAGCT 180
QY 181 TTGATGCTACCACTCCCTGGATGACATGACACCATGCTGTTTTTTAAAGGGGAGTTGTGT 240

Db	181	TTGATCTCACCACCTGGATGACAAATGGAAACATGCTGTTTAAAGGGGAGTTGTGT	240
Qy	241	GGAAAGTCAAAATGGGACCGGAGTTAATCTCAGAGAGTGGAGAAATTTCCCCAGCC	300
Db	241	GGAAAGTCAAAATGGGACCGGAGTTAATCTCAGAGAGTGGAGAAATTTCCCCAGCC	300
Qy	301	CTGTGGATGCTGCAATTCCTCAAGGTCAACAAGTGTCTTTCTGATCAAGGGGACAAAG	360
Db	301	CTGTGGATGCTGCAATTCCTCAAGGTCAACAAGTGTCTTTCTGATCAAGGGGACAAAG	360
Qy	361	TCGTGGGTATACCTCTCGAAAGAGGAGAAAGATACCCAAAGTTGCTCCAAAGATGAAT	420
Db	361	TCGTGGGTATACCTCTCGAAAGAGGAGAAAGATACCCAAAGTTGCTCCAAAGATGAAT	420
Qy	421	TTCTCTGGAATCCCATCCCACTGCGATGCGAATGTGGAAATGTCAACCTGGAGATGTCAAG	480
Db	421	TTCTCTGGAATCCCATCCCACTGCGATGCGAATGTGGAAATGTCAACCTGGAGATGTCAAG	480
Qy	481	CTGAAGCGGTCTCTTCTTCCAAAGGCATGGACAACAGGAATGGGACCTGGGCATCGGAACA	540
Db	481	CTGAAGCGGTCTCTTCTTCCAAAGGCATGGACAACAGGAATGGGACCTGGGCATCGGAACA	540
Qy	541	GTACCCACCATGGCCCTGAGTATATGGCTGTAGCCACACTAGTCTCTGCACTGA	600
Db	541	GTACCCACCATGGCCCTGAGTATATGGCTGTAGCCACACTAGTCTCTGCACTGA	600
Qy	601	CGTCTGACAAACCATGGTGCCACCTATGCCCTTCAGTGGGACCCACTACTGGCGTCTGGACA	660
Db	601	CGTCTGACAAACCATGGTGCCACCTATGCCCTTCAGTGGGACCCACTACTGGCGTCTGGACA	660
Qy	661	CCAGCCGGATGGCTGCGATAGTGGCCCATGTCTCATGTAGTGGCCCGGCTCTTCAG	720
Db	661	CCAGCCGGATGGCTGCGATAGTGGCCCATGTCTCATGTAGTGGCCCGGCTCTTCAG	720
Qy	721	CAGTGGATGCTGCCCTTTCTTGGGAAAGAAAACCTATCTGGTCCAGGGCAACCCAGTAT	780
Db	721	CAGTGGATGCTGCCCTTTCTTGGGAAAGAAAACCTATCTGGTCCAGGGCAACCCAGTAT	780
Qy	781	ATGTCCTCTGACAAAGGGAGCTATACCTAGTAGCGGTATCCCAAGCGGTGAGA	840
Db	781	ATGTCCTCTGACAAAGGGAGCTATACCTAGTAGCGGTATCCCAAGCGGTGAGA	840
Qy	841	AGGAAGTCGGACCCCTCATGGGATATCCTTGGACTCTGTGGATGCGGCTTTATCTGCC	900
Db	841	AGGAAGTCGGACCCCTCATGGGATATCCTTGGACTCTGTGGATGCGGCTTTATCTGCC	900
Qy	901	CTGGGTCTTCTGGCTCCATATCATGACGACGACGGCGCTGTGTGCTCGACCTGAAGT	960
Db	901	CTGGGTCTTCTGGCTCCATATCATGACGACGACGGCGCTGTGTGCTCGACCTGAAGT	960
Qy	961	CAGGAGCCCAAGCCAACGTGGACACAGCTTCCTGGGCCCTCATGAAAGGTAGACGGAGCCT	1020
Db	961	CAGGAGCCCAAGCCAACGTGGACACAGCTTCCTGGGCCCTCATGAAAGGTAGACGGAGCCT	1020
Qy	1021	TGTGTATGGAAGAAGTCCCTTGGCCCTTAATCTCATGTTCCGCCAATGGTCCCGGCTTGACC	1080
Db	1021	TGTGTATGGAAGAAGTCCCTTGGCCCTTAATCTCATGTTCCGCCAATGGTCCCGGCTTGACC	1080
Qy	1081	TCATCCATGGTCCCAATTTGTACTGTCTACGTGATGTGGAGAAACTCAATGACGACCAAGG	1140
Db	1081	TCATCCATGGTCCCAATTTGTACTGTCTACGTGATGTGGAGAAACTCAATGACGACCAAGG	1140
Qy	1141	CCCTTCCGCAACCCCAAGATGTGACAGGTCTCTGGGCTGCATCTACTGAGGGGCTTCT	1200
Db	1141	CCCTTCCGCAACCCCAAGATGTGACAGGTCTCTGGGCTGCATCTACTGAGGGGCTTCT	1200
Qy	1201	GACATGATCTGGCTGGCCCAACCTCTAGTTCTCTCATATAAAGACAGATGCTCTT	1260
Db	1201	GACATGATCTGGCTGGCCCAACCTCTAGTTCTCTCATATAAAGACAGATGCTCTT	1260
Qy	1261	CGCTTCTCACTAGGGGGCTTCTGACATGAGTCTGGCTGGCCCACTCCCAAGTTTCT	1320

QY	2401	ACCCAGACTGTGGCTCATGGCCCTCATGTGATCTGGAGTCAGGCCCTCCCACTGCTGCAGC	2460
DB	2401	ACCCAGACTGTGGCTCATGGCCCTCATGTGATCTGGAGTCAGGCCCTCCCACTGCTGCAGC	2460
QY	2461	CATTTCCTCCGTAGGACTTTGATGGGTAGAGTAGTAGCTAAACAAGCTCTGACTGTCAACAC	2520
DB	2461	CATTTCCTCCGTAGGACTTTGATGGGTAGAGTAGTAGCTAAACAAGCTCTGACTGTCAACAC	2520
QY	2521	AAGGCTTTGTACTGGGAGGCGCAGGCTATAGATGGCTCCAGCTTAAAGGGCTGGGAGCTG	2580
DB	2521	AAGGCTTTGTACTGGGAGGCGCAGGCTATAGATGGCTCCAGCTTAAAGGGCTGGGAGCTG	2580
QY	2581	GGGGACAGTGTCTCAGATTAGGGTCTAACTPAGGAAGTGTACTTGGAGCTCAGAACACAGGT	2640
DB	2581	GGGGACAGTGTCTCAGATTAGGGTCTAACTPAGGAAGTGTACTTGGAGCTCAGAACACAGGT	2640
QY	2641	TAGGGGCCAAGCAGCAGGGTGTGGGTCTACTCCTTAGGAGCACTTGAAGCTTTACTTTTT	2700
DB	2641	TAGGGGCCAAGCAGCAGGGTGTGGGTCTACTCCTTAGGAGCACTTGAAGCTTTACTTTTT	2700
QY	2701	CATTCTTAATGGTGTCTTGGATGGCTACCCCTCAGGGGTGTGGTGTCTAGTCTTAAGGGGTG	2760
DB	2701	CATTCTTAATGGTGTCTTGGATGGCTACCCCTCAGGGGTGTGGTGTCTAGTCTTAAGGGGTG	2760
QY	2761	GAGACAAGGACAGAGTTTTCAGGCTCGTCTCCTTATCAAGTTTCATGCACCTACACTTGGGACC	2820
DB	2761	GAGACAAGGACAGAGTTTTCAGGCTCGTCTCCTTATCAAGTTTCATGCACCTACACTTGGGACC	2820
QY	2821	ACTGCTGCATCAGCCAGGGAGCTCAGAGGTGTCTAAACAGTTTATCCACAACCTGTGATA	2880
DB	2821	ACTGCTGCATCAGCCAGGGAGCTCAGAGGTGTCTAAACAGTTTATCCACAACCTGTGATA	2880
QY	2881	CCCAAGGTTAACTTTTCTCTGTTTTCAGAGCGAGGAGTAGTACTAAGTCTCCCTTTCTCCT	2940
DB	2881	CCCAAGGTTAACTTTTCTCTGTTTTCAGAGCGAGGAGTAGTACTAAGTCTCCCTTTCTCCT	2940
QY	2941	TTCTCTCCACGTGTTCTCTTTCAGGGGAATCCTCTAGCTTCCTCTCCAGGGAATCCCCAGAA	3000
DB	2941	TTCTCTCCACGTGTTCTCTTTCAGGGGAATCCTCTAGCTTCCTCTCCAGGGAATCCCCAGAA	3000
QY	3001	ATGCTTTGTTTTCAGTCAGTTTAGCTGCTATATAGAGAAATCTTTAGAGTCGGGTAACTAT	3060
DB	3001	ATGCTTTGTTTTCAGTCAGTTTAGCTGCTATATAGAGAAATCTTTAGAGTCGGGTAACTAT	3060
QY	3061	CAGCAATAGGAATTTATGTTTCACAATCTGGAGGCTGGAAATCCCAAGATCAAGGCTCC	3120
DB	3061	CAGCAATAGGAATTTATGTTTCACAATCTGGAGGCTGGAAATCCCAAGATCAAGGCTCC	3120
QY	3121	AGCAGGTTTCAGTGTCTGCTGAGTGCCTTGTGTTCTGCTTCCAGAGATGGCAACCTTTTGTGCTG	3180
DB	3121	AGCAGGTTTCAGTGTCTGCTGAGTGCCTTGTGTTCTGCTTCCAGAGATGGCAACCTTTTGTGCTG	3180
QY	3181	TTCTCA 3186	
DB	3181	TTCTCA 3186	

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RESULT 2
US-09-900-448-3
; Sequence 3, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
; APPLICANT: CECCARDI, Toni et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001272
; CURRENT APPLICATION NUMBER: US/09/900,448
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fas-SEQ for Windows Version 4.0
; SEQ ID NO 3

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FILE REFERENCE: 791CIP2A
CURRENT APPLICATION NUMBER: US/10/105,891
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: 09/668,317
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 91
SOFTWARE: pt_genes Version 2.0
SEQ ID NO 19
LENGTH: 1631
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (71)..(1459)
US-10-105-891-19

Query Match 35.5%; Score 1129.8; DB 15; Length 1631;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1354; Conservative 0; Mismatches 2; Indels 213; Gaps 1;
QY 1 CTCCTGAGCTCAGCATGCTAGGTAAGTGGAGACCCGCTTGCCTGGGTTGTGGAGCC 60
DB 57 CTCCTGAGCTCAGCATGCTAGGTAAGTGGAGACCCGCTTGCCTGGGTTGTGGAGCC 116
QY 61 TATGCTGGTCTCTGGCCATTGGCCACCCCTTCTCCGACTAGTGGCCCATGGGAATGTTG 120
DB 117 TATGCTGGTCTCTGGCCATTGGCCACCCCTTCTCCGACTAGTGGCCCATGGGAATGTTG 176
QY 121 CTGAAGGGGAGACCAAGCCAGACCCAGACCTGTA CTGAAGCGTCTCAGATGGCTGGAGCT 180
DB 177 CTGAAGGGGAGACCAAGCCAGACCCAGACCTGTA CTGAAGCGTCTCAGATGGCTGGAGCT 236
QY 181 TTGATGCTACCACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 237 TTGATGCTACCACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 296
QY 241 GGAAGAGTCACAAATGAGGACCGGAGTTAATCTCAGAGATGAGAAATTTCCCCAGCC 300
DB 297 GGAAGAGTCACAAATGAGGACCGGAGTTAATCTCAGAGATGAGAAATTTCCCCAGCC 356
QY 301 CTGTGGATGCTGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 357 CTGTGGATGCTGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 416
QY 361 TCTGGGTATACCTCTGAAAGAGGAGAAAGATACCCAAAGTTGCTCCAGATGAAT 420
DB 417 TCTGGGTATACCTCTGAAAGAGGAGAAAGATACCCAAAGTTGCTCCAGATGAAT 476
QY 421 TTCTCTGGAATCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCAT 480
DB 477 TTCTCTGGAATCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCAT 536
QY 481 CTGAAGGGGCT 502
DB 537 CTGAAGGGGCT 596
QY 503 ----- 502
DB 597 CCATGAGGAGGCTTCTGCGGAGCTGTGCGGAGTCTCTCTGCGCTCTGAGTGGCTGG 656
QY 503 ----- 502
DB 657 GCGGCTACTACTGCTTCCAGGTAACCAATTCCTGCGCTTCCGACCTCTGAGGAGAGG 716
QY 503 -----AGGCC 507
DB 717 TGCCTCCAGGTACCCCGGGGATGTCGAGACTACTTCTGATGCTGCTGCGCTGCGGAGGCC 776
QY 508 ATGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCAGCTGCGCTGAGTATGTC 567
DB 777 ATGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCAGCTGCGCTGAGTATGTC 836

RESULT 5

US-10-162-335-87
; Sequence 87, Application US/10162335
; Publication NO. US20040009480A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Hjalt, Tord

QY 568 GCTGTAGCCCACTAGTCTTGTCTGCACTGACCTGCAACCACTGCTGCACTGCTGCACTGCTG 627
DB 837 GCTGTAGCCCACTAGTCTTGTCTGCACTGACCTGCAACCACTGCTGCACTGCTGCACTGCTG 896
QY 628 CTTTCACTGGGACCCCACTAGTCTTGTCTGCACTGACCTGCAACCACTGCTGCACTGCTGCACTG 687
DB 897 CTTTCACTGGGACCCCACTAGTCTTGTCTGCACTGACCTGCAACCACTGCTGCACTGCTGCACTG 956
QY 688 CCAATTGCTCATCAGTGGGCTGCTTGGGCTGCTTGGGCTGCTTGGGCTGCTTGGGCTGCTTGGGCT 747
DB 957 CCAATTGCTCATCAGTGGGCTGCTTGGGCTGCTTGGGCTGCTTGGGCTGCTTGGGCTGCTTGGGCT 1016
QY 748 AAAAATCTATCTGCTTCCAGGCAACCCAGGCTATGCTTCTGCACTGCTGCACTGCTGCACTGCTG 807
DB 1017 AAAAATCTATCTGCTTCCAGGCAACCCAGGCTATGCTTCTGCACTGCTGCACTGCTGCACTGCTG 1076
QY 808 CCTTAGTAAGCGGTTATCCGAAGCGGCTGGAAGGAGTGGGAGCCCTCATGGGATTA 867
DB 1077 CCTTAGTAAGCGGTTATCCGAAGCGGCTGGAAGGAGTGGGAGCCCTCATGGGATTA 1136
QY 868 TCTTGGACTCTTGGATGGGCTTATCTGCTTGGGCTTATCTGCTTGGGCTTATCTGCTTGGGCTTATCTG 927
DB 1137 TCTTGGACTCTTGGATGGGCTTATCTGCTTGGGCTTATCTGCTTGGGCTTATCTGCTTGGGCTTATCTG 1196
QY 928 CAGGACGGCGGCTGTGGTGGCTTGAACCTGGAAGTCAAGGAGCCCAAGCCACCTGGAAGGCTGGAAGG 987
DB 1197 CAGGACGGCGGCTGTGGTGGCTTGAACCTGGAAGTCAAGGAGCCCAAGCCACCTGGAAGGCTGGAAGG 1256
QY 988 TTCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 1047
DB 1257 TTCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 1316
QY 1048 ACTCATGTTCCGCCAATGCTCCGCTTGTACTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107
DB 1317 ACTCATGTTCCGCCAATGCTCCGCTTGTACTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1376
QY 1108 ACAGTATGTTGAGAACTGAAATGAGGAGCCCTTCCGGAACCCCAAGGAGGCTGGAAGGCTGGAAGG 1167
DB 1377 ACAGTATGTTGAGAACTGAAATGAGGAGCCCTTCCGGAACCCCAAGGAGGCTGGAAGGCTGGAAGG 1436
QY 1168 GTCTCTGGGCTGCACTCACTGAGGCGGCTTCTGACATGAGTCTGAGGCTGAGGCTGAGGCTGAGGCT 1227
DB 1437 GTCTCTGGGCTGCACTCACTGAGGCGGCTTCTGACATGAGTCTGAGGCTGAGGCTGAGGCTGAGGCT 1496
QY 1228 CTAGTCTCTCATATAAAGACAGATGCTTCTGCTTCTCTGCTTCTCTGCTTCTCTGCTTCTCTGCTTCT 1287
DB 1497 CTAGTCTCTCATATAAAGACAGATGCTTCTGCTTCTCTGCTTCTCTGCTTCTCTGCTTCTCTGCTTCT 1556
QY 1288 TGAGTCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 1347
DB 1557 TGAGTCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 1616
QY 1348 TTGAATCAA 1356
DB 1617 TTGAATCAA 1625

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APPLICANT: Kekuda, Ramesh
APPLICANT: Li, Li
APPLICANT: MacDougall, John R.
APPLICANT: Maliyankar, Uziel M.
APPLICANT: Millet, Isabelle
APPLICANT: Padigaru, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol E. A.
APPLICANT: Rastelli, Luca
APPLICANT: Shimkets, Richard A.
APPLICANT: Stone, David J.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Voss, Edward Z.
APPLICANT: Zernusen, Bryan D.
TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
FILE REFERENCE: 21402-377 B
CURRENT APPLICATION NUMBER: US/10/162.335
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/295,607
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/295,661
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/296,418
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/297,414
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/297,567
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/298,285
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/298,556
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/299,949
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/300,883
PRIOR FILING DATE: 2001-06-26
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 201
SEQ ID NO 87
LENGTH: 861
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (10)..(775)
US-10-162-335-87

Query Match
Best Local Similarity 20.2%; Score 644.8; DB 16; Length 861;
Matches 661; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 587 CTGTGCTGCACTGACGTCTGACACCATGCTGCCACCTATGCTTCAGTGGGACCCACTA 646
DB 174 CTTTGATGCTACACCTGGATGACATGGAACCACTGCTTTTAAAGGACCCACTA 233
QY 647 CTGGCGCTCTGGACACAGCCGGGATGGCTGGCATAGCTGGCCCATTCCTCATCAGTGGCC 706
DB 234 CTGGCGCTCTGGACACAGCCGGGATGGCTGGCATAGCTGGCCCATTCCTCATCAGTGGCC 293
QY 707 CAGGGTCTTTCAGTGGATGCTGCTTTCCTGGGAGAAACTCTATCTGGTCCA 766
DB 294 CCAGGGTCTTTCAGTGGATGCTGCTTTCCTGGGAGAAACTCTATCTGGTCCA 353
QY 767 GGGCACCCAGGTATATGTTCTTCTGCAAAAGGAGGCTATACCTAGTAGGGGTTATCC 826
DB 354 GGGCACCCAGGTATATGTTCTTCTGCAAAAGGAGGCTATACCTAGTAGGGGTTATCC 413
QY 827 GAAGCGGCTGGAGAGAGAGTGGGACCCCTCATGGGATATACCTGGAATCTGTGGATGC 886
DB 414 GAAGCGGCTGGAGAGAGAGTGGGACCCCTCATGGGATATACCTGGAATCTGTGGATGC 473
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887 GGCCTTTATCTGCCCTGGGTCTTCTCGGTCCCATATCATGCGAGGACGGGGCTGTGGTG 946
474 GGCCTTTATCTGCCCTGGGTCTTCTCGGTCCCATATCATGCGAGGACGGGGCTGTGGTG 533
947 GCTGGACCTCAAGTCAAGAGGCCCAAGCCAGTGGAGAGAGCTTCTTGGCCCCCATGAGAA 1006
534 GCTGGACCTCAAGTCAAGAGGCCCAAGCCAGTGGAGAGAGCTTCTTGGCCCCCATGAGAA 593
1007 GGTAGAGGAGGCTTGTATGGAAGTCCCTTGGCCCTAACTCATGTTCCGCAATGG 1066
594 GGTAGAGGAGGCTTGTATGGAAGTCCCTTGGCCCTAACTCATGTTCCGCAATGG 653
1067 TCCGGCTTCTTACTCTCATCCATGCTCCCAATTTGTACTGCTACAGTATGAGAGAACT 1126
654 TCCGGCTTCTTACTCTCATCCATGCTCCCAATTTGTACTGCTACAGTATGAGAGAACT 713
1127 GAATGAGGAGGCTTCTTGGGACCCAGGATGTGACAGTCTCTTGGGCTGCATCTCA 1186
714 GAATGAGGAGGCTTCTTGGGACCCAGGATGTGACAGTCTCTTGGGCTGCATCTCA 773
1187 CTGAGGGGCTTCTGACATGAGTCTGCTGCTGGCCCTGGCCCACTCTCTAGTTTCTCATATAAG 1246
774 CTGAGGGGCTTCTGACATGAGTCTGCTGCTGGCCCTGGCCCACTCTCTAGTTTCTCATATAAG 833
1247 ACAGATTGCTTCTTGGCTTCTTCTACTGAG 1274
834 ACAGATTGCTTCTTGGCTTCTTCTACTGAG 861

RESULT 6
US-10-175-523-84
; Sequence 84, Application US/10175523
; Publication No. US20030096264a1
; GENERAL INFORMATION:
; APPLICANT: Brockman, Jeffrey
; APPLICANT: Evans, David
; APPLICANT: Hook, Derek
; APPLICANT: Klimczak, Leszek
; APPLICANT: Laeng, Pascal
; APPLICANT: Palfreyman, Michael
; APPLICANT: Rajan, Priithi
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
; FILE REFERENCE: 3235/LJ795-US3
; CURRENT APPLICATION NUMBER: US/10/175,523
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,151
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 84
; LENGTH: 1516
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-175-523-84

Query Match
Best Local Similarity 18.1%; Score 576.8; DB 15; Length 1516;
Matches 999; Conservative 0; Mismatches 257; Indels 228; Gaps 4;

QY 1 CTCTCAGCTCAGCATGCTAGGGTACTGGGAGGACCCGTTGCATCTGGGTTGTGGAGCC 60
DB 41 CTTTCAGCTCCCATGGCTAGGACGATAGTACACTAAATATCTGTATTGCTGGGCC 100
```


241 GGAAGAGTCACAAATGGGACCGGAGTAAATCTCAGAGAGATGGAGAATTTCCCGAGCC 300
Db |||||
281 GGAAGGCTCCTCAGGATCCGGAATTAATCTCAGAGAGATGGAGAATTCGGTCACT 340
Qy |||||
301 CTGTGATGCTGCAATTCGCTCAAGGTCAACAGAGTCTCTTTCTGATCAAGGGGCAAG 360
Db |||||
341 CAGTGGATGCTGCAATTCGCTCAAGGTCAACAGAGTCTCTTTCTGATCAAGGGAAGCA 397
Qy |||||
361 TCTGGGTATACCTCTCTGAAAGAGGAGGATACCAAGTTGCTCCAGATGAT 420
Db |||||
398 TCTGGGTATACCTCTCTGAAAGAGGAGGATACCAAGTTGCTCCAGATGAT 457
Qy |||||
421 TTCTCTGGAATCCCATCCCACTGATGAGTGTGGAATGTCAACCTGGAGAAATGTCAAG 480
Db |||||
458 CTCTCTGGAATCCCATCCCACTGATGAGTGTGGAATGTCAACCTGGAGAAATGTCAAG 517
Qy |||||
481 CTGAGGGCTCTCTCTCTCAAGGCA----- 508
Db |||||
518 GTGAAGGTGCTCTCTCTCTCAAGGTAACCGCAAGTGTCTGGGACTTTGGCAACAAGAA 577
Qy |||||
509 ----- 508
578 CCCAAAGAAAGTTCCTGGCTGCTGTTGGGAAATGGCACTGGGCTTTGAGGTGCTTG 637
Db |||||
509 ----- 508
638 AACGCTACTGCTTCCAGGGTAACAAGTCTCTGAGATTTAAACCCCGTCACAGAGAGG 697
Qy |||||
509 ----- 508
698 TGCTCTCCAGATACCTCTGGATGCGCGTGAATCTCTATATATCTGCTGCGAGAGGCC 757
Qy |||||
509 -----TGCAACAGAGTACCTGGCAACAGTACCCACCATGCGCTGAGTATA 564
Db |||||
758 ATGGTAACTAAGAAATGGAATCTCTCATGGGAATAGCACCA-----TCTATGCAAT 811
Qy |||||
565 TGGCTGTAGCCACATCTAGTCTTGTCTGCACTGAGCTGTGACACCATGAGTGGCACT 824
Db |||||
812 CGCGTTGTAACGAGATCTCGGCTGCTGCACTGCTGTGACCATGAGGAGTCACT 871
Qy |||||
625 ATGCTTCTAGTGGACCACTACTGCGTCTGACACCAAGCGGATGCTGCTGATAGCT 684
Db |||||
872 ATGCTTCTAGTGGTCCCACTACTGCGTCTGACCTCGAGTGGTGGTGGTGGTGGT 931
Qy |||||
685 GCGCCATGCTATCAATAGTGGCCCAAGGCTCTTCAAGAGTGGATGCTGCTTCTGGG 744
Db |||||
932 GCGCCATGCTATCAATAGTGGCCCAAGGCTCTTCAAGAGTGGATGCTGCTTCTGGG 991
Qy |||||
745 AGAAGAACTCTATCTGCTGAGGCAAGGCTATATGCTCTTCTGACAAAGGGAGGCT 804
Db |||||
992 ATGAGAAAGTCTATCTGATCCAGGCACTGAGTATATGCTCTTCTGACGAGGGGCA 1051
Qy |||||
805 ATACCTTAGTAAGCGGTATCCGAAGCGGCTGAGAGGAGTTCGGGACCCCTCATGGGA 864
Db |||||
1052 ATACCTTAGTAAGCGGTATCCGAAGCGGCTGAGAGGAGTTCGGGACCCCTCATGGGA 1111
Qy |||||
865 TTATCTGAGTCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 924
Db |||||
1112 TCAGCTTGTATACCATAGATGCAAGCTTTCTGCGCTGGTCTTCTCAAGCTCTAGTCA 1171
Qy |||||
925 TGGCAGGACGCGGCTGTGCTGCTGAGCTGAGTTCAGAGCCCAAGCCAGCTGAGAG 984
Db |||||
1172 CATCAGGACGCGGCTGTGCTGCTGAGCTGAGTTCAGAGCCCAAGCCAGCTGAGAG 1231
Qy |||||
985 AGCTTCTTGGCCCATGAGAGAGTGTGAGAGGCTGTGATGAGAAAGTCTCTTGGCC 1044
Db |||||
1232 AGCTTCTTGGCCCATGAGAGAGTGTGATGAGTGTGATGAGAAAGTCTCTTGGCC 1291
Qy |||||
1045 CTAACTCATGCTTCCGCAATGCTGCGGCTGTGATCTTCTGATCTTCTGATCTTCTGAT 1104
Db |||||
1292 CTTACTCATGCTTCTTCAATGCTTCCCACTTGTCTTCTTCTTCTTCTTCTTCTTCTT 1351
Qy |||||
1105 GCTACAGTGTGAGGAACTGAATGTCAGGCAAGGCGCTTCCGCAACCCCAAGATGTGA 1164

1352 GCTATAGCAGTATACAGAACTGATGAGCAAGAGTCTGCTCAGCCCCAGAAAGTGA 1411
Qy |||||
1165 CCAGTCTCTCTGGCTGCACTCACTCAGGGCC--TCTGACATGAGTCTGCGCTGGCC 1221
Db |||||
1412 ACAGCATCTCTGGCTGCACTCAATAAAGCCCTGATGGGAATAGCCAGGCCACCCCA 1471
Qy |||||
1222 CACCTCTCTAGTCTCTCAATAAAGCAGAGTGTCTTCTTCTGCTT 1265
Db |||||
1472 CTTCTCCATTTCCATTTCTTANTAAACAGATGGTTCTTCTCAT 1515

RESULT 8

US-09-918-995-30828
; Sequence 30828; Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Eysseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30828
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(488)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-30828

Query Match 13.4%; Score 427; DB 10; Length 488;

Best Local Similarity 100.0%; Pred. No. 3.2e-131; Indels 0; Gaps 0;
Matches 427; Conservative 0; Mismatches 0;

Qy 5 GCAGCTCAGCATGCTAGGGTACTGGGAGCACTGGGAGTGTGAGGCTATG 64
Db 61 GCAGCTCAGCATGCTAGGGTACTGGGAGCACTGGGAGTGTGAGGCTATG 120
Qy 65 CTGGTCTCTGGCATTGCCACCCCTCTTCTCGAGTAGTGCCCATGGGAATGTGCTGA 124
Db 121 CTGGTCTCTGGCATTGCCACCCCTCTTCTCGAGTAGTGCCCATGGGAATGTGCTGA 180
Qy 125 AGGCGAGACCAAGCCAGACCCAGAGCTGCACTGAACCCCTGCTCAGATGGCTGAGCTTTGA 184
Db 181 AGGCGAGACCAAGCCAGACCCAGAGCTGCACTGAACCCCTGCTCAGATGGCTGAGCTTTGA 240
Qy 185 TGCTACCACTCTGGATGCAATGGAAACCATGCTGTTTTTAAAGGGGAGTTTGTGTGAA 244
Db 241 TGCTACCACTCTGGATGCAATGGAAACCATGCTGTTTTTAAAGGGGAGTTTGTGTGAA 300
Qy 245 GAGTCACAAATGGGACCGGAGTTAATCTCAGAGAGATGGAGATTTCCCGAGCCCTGT 304
Db 301 GAGTCACAAATGGGACCGGAGTTAATCTCAGAGAGATGGAGATTTCCCGAGCCCTGT 360
Qy 305 GGATCTGCTGATTTCCCTCAAGGTCAACACAGTGTCTTCTGATCAAGGGGGAACAAAGTCTG 364
Db 361 GGATCTGCTGATTTCCCTCAAGGTCAACACAGTGTCTTCTGATCAAGGGGGAACAAAGTCTG 420
Qy 365 GGTATACCTCTCTGAAAGAGGAGAAAGATACCAAGTTGCTCCAGATGAAATTTCC 424
Db 421 GGTATACCTCTCTGAAAGAGGAGAAAGATACCAAGTTGCTCCAGATGAAATTTCC 480
Qy 425 TGGATC 431
Db 481 TGGATC 487

Query Match 11.7%; Score 374.2; DB 10; Length 488;
Best Local Similarity 99.2%; Pred. No. 1.5e-113;
Matches 376; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 503 AGGCATGACACAGGAATGGAGCTGGCCATGGGAAAGAGTACCCACCATGGCCCTGAGTA 562
DB 110 AGGCATGACACAGGAATGGAGCTGGCCATGGGAAAGAGTACCCACCATGGCCCTGAGTA 169
QY 563 TATGGCTGTAGCCACATCTAGTCTTCTGTGCACTGACGCTCTGACACCATGGTGGCCAC 622
DB 170 TATGGCTGTAGCCACATCTAGTCTTCTGTGCACTGACGCTCTGACACCATGGTGGCCAC 229
QY 623 CTATGCCCTTCAGTGGGACCCACTACTGGCGCTTGGACACCGCCGGGATGCTGGCATAG 682
DB 230 CTATGCCCTTCAGTGGGACCCACTACTGGCGCTTGGACACCGCCGGGATGCTGGCATAG 289
QY 683 CTGGCCCATCTCATAGTGGCCGCCAGGCTCTTCCAGCTGGATGCTGCTTTCTG 742
DB 290 CTGGCCCATCTCATAGTGGCCGCCAGGCTCTTCCAGCTGGATGCTGCTTTCTG 349
QY 743 GGAAGAAAACCTCTATCTGGTCCAGGACCCAGGTATATGTCTTCTTGACAAAGGGAGG 802
DB 350 GGAAGAAAACCTCTATCTGGTCCAGGACCCAGGTATATGTCTTCTTGACAAAGGGAGG 409
QY 803 CTATACCCCTAGTACCGGTATCCGAGCGGCTGGAGAGGAGTCCGGACCCCTCATGG 862
DB 410 CTATACCCCTAGTACCGGTATCCGAGCGGCTGGAGAGGAGTCCGGACCCCTCATGG 469
QY 863 GATTATCTGGACTCTGTG 881
DB 470 GATTATCTGGACTCTGTG 488

RESULT 12
US-09-918-995-32820
; Sequence 32820, Application US/09918995
; Publication No. US200300736231
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32820
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(491)
; OTHER INFORMATION: c = A,T,C or G
US-09-918-995-32820

Query Match 10.8%; Score 345.4; DB 10; Length 491;
Best Local Similarity 99.7%; Pred. No. 6.3e-104;
Matches 346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 503 AGGCATGACACAGGAATGGAGCTGGCCATGGGAAAGAGTACCCACCATGGCCCTGAGTA 562
DB 145 AGGCATGACACAGGAATGGAGCTGGCCATGGGAAAGAGTACCCACCATGGCCCTGAGTA 204
QY 563 TATGGCTGTAGCCACATCTAGTCTTCTGTGCACTGACGCTCTGACACCATGGTGGCCAC 622
DB 205 TATGGCTGTAGCCACATCTAGTCTTCTGTGCACTGACGCTCTGACACCATGGTGGCCAC 264
QY 623 CTATGCCCTTCAGTGGGACCCACTACTGGCGCTTGGACACCGCCGGGATGCTGGCATAG 682
DB 265 CTATGCCCTTCAGTGGGACCCACTACTGGCGCTTGGACACCGCCGGGATGCTGGCATAG 324

RESULT 13

US-09-880-107-3166/c

; Sequence 3166, Application US/09880107

; Patent No. US20020142981A1

; GENERAL INFORMATION:

; APPLICANT: Horne, Darci T.

; APPLICANT: Vockley, Joseph G.

; APPLICANT: Schert, Uwe

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

; FILE REFERENCE: 44921-5028-WO

; CURRENT APPLICATION NUMBER: US/09/880,107

; CURRENT FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: US 60/211,379

; PRIOR FILING DATE: 2000-06-14

; PRIOR APPLICATION NUMBER: US 60/237,054

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 3950

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3166

; LENGTH: 504

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(504)

; OTHER INFORMATION: n = a or c or g or t

; OTHER INFORMATION: Genbank Accession No. US20020142981A1 T61801

US-09-880-107-3166

Query Match

Best Local Similarity 91.4%; Score 313.4; DB 9; Length 504;

Matches 468; Conservative 0; Mismatches 29; Indels 15; Gaps 13;

QY 839 GAAGAAAGTCGGACCCCTCATGGGATATCTCGACTCTCTGGATCGGCTTTATCTG 898
DB 498 GAAAGAAAGTGGACCCCTCATGGGATATCTCGACTCTCTGGATCGGCTTTATCTG 440
QY 899 CCCTGGGTCTTCTCGCTCCATATCATGGCAGGACGGGGCTGTGGCTGGACCTGAA 958
DB 439 CCCT-GGTCCTTCTCGCTCCATATCATGGGAGGAGCGCTGTGGCTGGACCTGAA 381
QY 959 GTCAGGAGCCCAAGCCAGCTGGACAGAGCTTCCCTGG-CCCCATGAGAGGTAGCGAG 1017
DB 380 GTCAGGA-NCCAAGCCAGCTGGANAGAGCTTCCCTGGNCCCCCATGAGAGGTAGCGAG 322
QY 1018 CTTGTGTATGGAAGAGTCCCTCGCCCTACTCATGTTCGCCAAATGGTCCCGCTTGT 1077
DB 321 CTTGTGTATGGAAGAGNC-CTTGGCCCTAACTCATGTTCGCCAAATGGTCCCGCTTGT 263
QY 1078 ACCTCATCCATGGTCCCAATTTGTACTGCTACAGTATGTGGAGAACTGAATGACGCA 1137
DB 262 ACCTCATCCATGG-CCCAATTTGTACTGCTANAGTATGTGGAGAACTGAATGCA-NCA 205
QY 1138 AGGCCCTTCCCAACCCAGAGATGTGACAGTCTTCCGGCTGCACTCACTGAGGGGCT 1197
DB 204 AGGCCCTTCCCAACCCAGAGATGTGACAGTCTTCCGGCTGCACTCACTCACTCA-GGGCT 146
QY 1198 TCTGACATGATGTGGCTCGGCCCTCGGCCACCTCTCTAGTTTCTCTATAATAAGACAGATTTGCT 1257

Db 145 TCTGATGAGTCTG--CTGGCCACCTCTCTAG--TCCTCATATATATAGACAGATTGCTT 89
QY 1258 CTTGCTCTTCTCACTAGGCGCCTTCTGACATAGTCTGCGCTGGCCCACTCCCACTT 1317
Db 88 CTT-GCTTCTCACTGA-GGCGCTTCTGACATGAGTCTG--CCTGCGCCCACTCCCACTT 33
QY 1318 TCTCATATATATAGACAGATTGCTTCTTCACTT 1349
Db 32 TCTCATATATATAGACAGATTGCAATTTCACCT 1
RESULT 14
US-09-960-352-10323
; Sequence 10323, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Mathialagan, Nagabhan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 10323
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 44-LIB34-041-Q1-E1-C8
US-09-960-352-10323

Query Match 9.4%; Score 298.4; DB 9; Length 420;
Best Local Similarity 81.9%; Pred. No. 3e-88;
Matches 344; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
QY 663 AGCCGGATGGCTGGCATAGCTGGCCCATTTGCTCATCAGTGGGCCCAAGGTCCTTGAACA 722
Db 1 AGCCGGACGGGTGGCACAGCTGGCTCATTTAGCATCTGTGGGCCCAAGGTCCTTCAACA 60
QY 723 GTGATGCTGCTTCTTCTGGGAGAAACTCTATCTGTGTCAGGSCACCCAGGTATAT 782
Db 61 GTGATGCTGCTTCTTCTGGGATAAAGCTCTACCTCATTCAGGTATCCAGGTATAT 120
QY 783 GTCTTCTGACAAAGGAGGCTATACCTATATAGCGGTTATCCGAAGCGGCTGGAGAAG 842
Db 121 ATCTTCTGACAGGCGAGGCTACACTCTGTAAGATTATCCAAAGCAGCTGGAGAAG 180
QY 843 GAATGCGGACCCCTCATATGAGGATTTATCTGAGCTCTGTGATGGGCTTTATCTGCTCT 902
Db 181 GAATTTGGAGCCCTGATGGGCTCTGCTTCAATCTGTGATGAGGCTTTACCTGTCTT 240
QY 903 GGGTCTTCTGCGCTCCATATCATGCGAGGAGCGGCTGTGCTGGCTGGACCTGAAGTCA 962
Db 241 GATCTTCTGAGCTTACATCATGCGACCCAGAGCTGTGGAGCTGGACCTGAAGTCA 300
QY 963 GAGGCCAAGCCAGCTGACAGAGCTTCTTTGGCCCAATGAGAGGTAGACGAGCTTG 1022
Db 301 GGAGCTCAAGCCAGCTGACAGAGCTTCTTTGGCTCCATACGAAGATCGATGGGGCCCTG 360
QY 1023 TGTATGGAAGAGTCCCTTGGCCCTTAACCTCATGTTCCGCCAATGTTCCCGGCTTGTACTTC 1082
Db 361 TGTACAGAGAAGTCTCTGGGCCCCCACCCTCGTGTCTGCAATGCTGGGGCTTGTACTTC 420

RESULT 15
US-09-960-352-7040
; Sequence 7040, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.

; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagabhan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 7040
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 30-LIB34-026-Q1-E1-H5
US-09-960-352-7040

Query Match 8.8%; Score 280; DB 9; Length 408;
Best Local Similarity 80.4%; Pred. No. 4.2e-82;
Matches 328; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY 767 GGGCACCCAGGTATATGCTTCTGACAAAGGAGGCTATACCTAGTAAGGGTTATCC 826
Db 1 GGGTACCCAGGTATATATCTTCTGACAAAGGAGGCTATACCTCGTAAAGATTATCC 60
QY 827 GAGCGGCTGGAGAGGAAGTGGGACCCCTCATGGGATTATCTCTGGACTCTGTGATGC 886
Db 61 AAGCAGCTGGAGAGGAATTGGGAGCCCTGATGGGGTCTGCCCTTCAATCTGTGATGC 120
QY 887 GGCCTTTATCTGCCCTTGGGCTCTTCTGGGCTCCATATCATGAGGACGGCGCTGTGTTG 946
Db 121 AGCCTTTACCTGCTCTGGATCTTCTCAGCTCTACATCATGCGAGCCAGAGCTGTGGAG 180
QY 947 GCTGACCTGAGTCAAGGACCCAGGACCGGAGCAGAGCTTCTTGGCCCCCATGAGAA 1006
Db 181 GCTGACCTGAACTTAGGAGCTCAAGCCACGAGGACAGCTTCTTGGCTCCATACGAA 240
QY 1007 GGTAGACGAGGCTTGTGTATGAAAAGTCCCTTGGCCCTAACTCATGTTCCGCAATGG 1066
Db 241 AGTCGATGGGCGCTGTGTACAGAGAAGTCTCTGGGCCCCCACTCTGTGTTCTGCCAATGG 300
QY 1067 TCCCGCTTGTACTCATTCATGTTGCCAATTTGTACTGTCTACAGTGTGAGAACT 1126
Db 301 TCTGGGCTTGTACTCTGTCGAAGGGCCCCAATCTGTACTGTCTAAGATGTGAGGAATT 360
QY 1127 GAATGACGACCAAGGCGCTTCCGCAACCCCAAGAAATGTGACAGTCTCTCT 1174
Db 361 GAGCAGACCAAGGAGCTTCCCGAGCCAGAGGATGAACAGCCTCTCT 408

Search completed: June 8, 2004, 06:00:01
Job time : 1300 secs

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OM nucleic - nucleic search, using sw model

Run on: June 8, 2004, 01:43:13 ; Search time 197 Seconds
(without alignments)
8974.993 Million cell updates/sec

Title: US-09-900-448-1
Perfect score: 3186
Sequence: 1 cctctgagctcagcatggtt.....accttttctgtgtcttca 3186

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	2.8	3001	4	US-09-539-333D-177
2	86	2.7	87350	3	US-08-781-891-79
3	86	2.7	87350	4	US-09-618-166-79
4	86	2.7	87543	4	US-09-791-211-3
5	83.2	2.6	503	4	US-09-621-976-3523
6	82.6	2.6	48763	4	US-09-916-204-3
7	82.6	2.6	174493	4	US-09-804-471A-3
8	82.6	2.6	174493	4	US-10-238-709-3
9	82.2	2.6	161652	4	US-09-497-855A-40
10	80.8	2.5	63588	4	US-09-873-404-3
11	80.4	2.5	50000	4	US-09-146-053-4
12	79.2	2.5	193303	4	US-09-497-855A-37
13	79.2	2.5	193303	4	US-09-497-855A-44
14	79	2.5	1001	4	US-09-671-317-212
15	79	2.5	1001	4	US-09-671-317-458
16	78.4	2.5	8353	3	US-08-611-587-1
17	77.6	2.4	72928	3	US-09-009-913-1
18	69.2	2.2	1282	4	US-09-205-258-197
19	69	2.2	50000	4	US-09-146-053-3
20	68.4	2.1	197496	4	US-08-877-177A-10
21	68.2	2.1	309	4	US-09-222-575-145
22	68.2	2.1	309	4	US-09-389-681-145
23	68.2	2.1	309	4	US-09-620-405B-145
24	68.2	2.1	309	4	US-09-339-338-145
25	68.2	2.1	309	4	US-09-433-826B-145
26	68.2	2.1	309	4	US-09-604-287A-145
27	68.2	2.1	309	4	US-09-285-480-145

Sequence 145, App
Sequence 4, Appli
Sequence 183, App
Sequence 183, App
Sequence 185, App
Sequence 185, App
Sequence 1, Appli
Sequence 459, App
Sequence 11, Appli
Sequence 14, Appli
Sequence 3, Appli
Sequence 20, Appli
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Sequence 192, App
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Sequence 1, Appli

US-09-834-759-145
US-09-146-053-4
US-09-640-173-183
US-09-713-550-183
US-09-640-173-185
US-09-713-550-185
US-09-536-059-1
US-09-641-638-459
US-10-027-983-11
US-08-232-463-14
US-09-751-389-3
US-08-724-394A-20
US-08-724-394A-21
US-08-724-394A-22
US-09-539-333D-192
US-09-146-053-5
US-09-539-333D-1
US-09-679-409-1

ALIGNMENTS

RESULT 1
US-09-539-333D-177
; Sequence 177, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Essioux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: GENSET.047AUS
; CURRENT APPLICATION NUMBER: US/09/539,333D
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/416,384
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent.pm
; SEQ ID NO 177
; LENGTH: 3001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1501
; OTHER INFORMATION: 99-15668-139 : polymorphic base C or T
; FEATURES:
; NAME/KEY: misc binding
; LOCATION: 1482..1500
; OTHER INFORMATION: 99-15668-139.mis1
; FEATURES:
; NAME/KEY: misc binding
; LOCATION: 1502..1521

OTHER INFORMATION: 99-15668-139.mis2, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 1363..1380
OTHER INFORMATION: upstream amplification primer
FEATURE:
NAME/KEY: primer bind
LOCATION: 1801..1821
OTHER INFORMATION: downstream amplification primer, complement
FEATURE:
NAME/KEY: misc binding
LOCATION: 1489..1513
OTHER INFORMATION: 99-15668-139 probe
US-09-539-333D-177

Query Match 2.8%; Score 88; DB 4; Length 3001;
Best Local Similarity 71.7%; Pred. No. 8.9e-18;
Matches 129; Conservative 0; Mismatches 50; Indels 1; Gaps 1;
QY 3008 GTTTCAGTCAGTTAGGCTGTATTAAGAGATATCTTAGAGTGGSTAATCTATCAGCAAT 3067
DB 2055 GTTCTAGTCAGTTTTCCTGCTGTAAACAAATACACAGACTGGTCTATTAATAAGAAG 2114
QY 3068 AGGAATTTATTTGTCACAAATCTCGAGGCTGGAATCCAGATCAAGGCTCCAGCAGGT 3127
DB 2115 AAGAAATCAATTTCTCAATAGTTCTGGAGGCTAGAAAGTCCGAGATGAAGGCGCCAGCAAT 2174
QY 3128 TCAGTGTCTGCTGAGTGTCT-TGTTCTGCTTCCAGAGTGGACCTTTTTCGTGTCTCA 3186
DB 2175 TTGGTGTCTGAGGGTGGCTCTCTCTCCAGATGAGCTTTGATGCTGCAATTTCA 2234

RESULT 2
US-08-781-891-79/c
Sequence 79, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781.891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620cunburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-781-891-79
Query Match 2.7%; Score 86; DB 3; Length 87350;
Best Local Similarity 73.3%; Pred. No. 4.8e-16;
Matches 151; Conservative 0; Mismatches 50; Indels 5; Gaps 3;
QY 2983 TCCAGGGAATCCCAAGAAAGTTTGTTCAGTCAGTTTAGGTGCT---ATAAGAGAAAT 3039
DB 68776 TACTAGTATGTCCAGAACTGATTTGTCTAGTCTGTTTTCATATACAAAAAT 68717
QY 3040 ATCTTAGAGTGGTAATCTATCAGCAATAGAAATTTATCTTCAATTTCTGGAGGCTGG 3099
DB 68716 GCCACGACTGGCAATTTTCAACACAGATGTTTATTTCTCATAGTTCTGGAGGCTGG 68657
QY 3100 AAATCCCAAGATCAAGGCTCCAGCAGGTTCAAGTCTGCTGAGTGCTTGT-TCTGCTTGG 3158
DB 68656 -AGGTCCCAAGATCAAGGCGCCAGTAGTTCAAGTCTGCTGAGGCTGCTCTCTGCTTCC 68598
QY 3159 AAGATGGCACCTTTTTCGTGTCTCT 3184
DB 68597 AAATGGAGGCTTTCGCTGTCTCT 68572
RESULT 3
US-09-618-166-79/c
Sequence 79, Application US/09618166
Patent No. 6583112
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/618.166
FILING DATE: 17-Jul-2000
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-618-166-79

Query Match 2.7%; Score 86; DB 4; Length 87350;
Best Local Similarity 73.3%; Pred. No. 4.8e-16;
Matches 151; Conservative 0; Mismatches 50; Indels 5; Gaps 3;

QY 2983 TCAGGGAATCCAGAAATGTTTTCAGTCAGTTAGGCTGCT---ATAAGAGAT 3039
Db 68776 TACTAGTATGTGCGCAGAACTGATTTGCTTAGTCTGTTTTCATACCAAAAT 68717
QY 3040 ATCTTAGAGTGGGTAACTATCAGCAATAGAAATTTATTTTCACAAATTCAGAGGCTGG 3099
Db 68716 GCCACAGACTGGCAATTTACAACAACAGTAGTTTATTTTCATAGTTCTGAGGCTGG 68657
QY 3100 AAAATCAAGATCAAGGCTCCAGAGTTCAGTCTGCTGAGTGCTGTG-TCGCTTTCG 3158
Db 68656 -AGGTCGAAGATCAAGGCGCAGTAGGTTTCAGTCTGCTGAGGCTGCTCTCTGCTTCC 68598
QY 3159 AGATGCGACCTTTTTCGCTGTCT 3184
Db 68597 AAAATGAGGCTTGTCGCTGTGCT 68572

RESULT 4
US-09-791-211-3/c
Sequence 3, Application US/09791211
Patent No. 6448080
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791.211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 3
LENGTH: 87543
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: 7421
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 7427
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 11609
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 12605
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 12742
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29370
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29422
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29979
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29980
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29981
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 30136
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 30140
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 31205
OTHER INFORMATION: unknown

NAME/KEY: unsure
LOCATION: 31206
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 31592
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 33095
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 33160
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 34066
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 34072
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 36816
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 39020
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 42164
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 42459
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46808
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46823
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46826
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 47291
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NAME/KEY: unsure
LOCATION: 52786
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 52787
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 53384
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 54684
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59215
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59235
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59242
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 63290
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 66614
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68660
OTHER INFORMATION: unknown
NAME/KEY: unsure


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; LOCATION: 68697
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68718
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68733
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 68739
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 69785
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 73134
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 79198
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 86336
; OTHER INFORMATION: unknown
; OTHER INFORMATION:
; US-09-791-211-3

Query Match          2.7%; Score 86; DB 4; Length 87543;
Best Local Similarity 73.3%; Pred. No. 4.8e-16;
Matches 151; Conservative 0; Mismatches 50; Indels 5; Gaps 3;

QY 2983 TCAGGGAACCTCCAGAAATGGTTTTCAGTCAGTTCAGTCTGCT---ATAAGAGAT 3039
DB 68969 TACTAGTATGTGCCAGACTGATTTCTTAGTCTGTTTCTGTTTTCATACACAAAT 68910

QY 3040 ACTTTAGAGTGGTATCTATCAGCAATAGGAATTTATTTGTTCCAAATTCAGAGCTCG 3099
DB 68909 GCCACAGACTGGCAATTTACAAACACAGTAGTATTTTCATAGTTCTCGAGGCTCG 68850

QY 3100 AAAATCCAGATCAAGGCTCCAGAGTCCAGAGTTCAGTGTCTGCTAGTCTGTTGT-TCTGCTTCG 3158
DB 68849 -AGGTCCAAGATCAAGGCGCCAGTAGGTTCAAGTGTCTGCTGAGGCTGCTCTCTGCTTCC 68791

QY 3159 AGAGTGCACCTTTTTCCTGCTGTCT 3184
DB 68790 AAAATGAGGCTTGTGCTGTGTCTCT 68765

RESULT 5
US-09-621-976-3523/c
; Sequence 3523, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3523
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 134..382
; US-09-621-976-3523

Query Match          2.6%; Score 83.2; DB 4; Length 503;
Best Local Similarity 75.7%; Pred. No. 9.2e-17;
Matches 103; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
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QY 3019 TTTAGGCTGCTATAAGAGAAATATCTTAGAGTGGTAAATCTATCAGCAATAGGAATTTAAT 3078
DB 386 TTTATGAGCTATACAGAAATACCTTAGCATGAGTAATATAATAATAAATAAATGATG 327
QY 3079 GTTCACAAATTCGAGGCTGGAATCCAGATCAAGGCTCCAGCAGTTCAGTGTCTGTC 3138
DB 326 TCTTACAGTCTCGAGGTTGAAAAATCCAGATCATGCGCACTGGCAGGTTTGTGCTGTC 267
QY 3139 TGAGTGTCTTGTCTGC 3154
DB 266 TGAGGCTGATCTTC 251
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RESULT 6

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US-09-916-204-3
; Sequence 3, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 48763
; TYPE: DNA
; ORGANISM: Human
; US-09-916-204-3

Query Match          2.6%; Score 82.6; DB 4; Length 48763;
Best Local Similarity 72.2%; Pred. No. 4.2e-15;
Matches 135; Conservative 0; Mismatches 49; Indels 3; Gaps 2;
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QY 3000 AATGTTTGTTCAGTCAGTTCAGTCTGCTATACAGAAATATCTTAGAGTGGTAAATCTA 3059
DB 15209 AAACGTGATCTGAGTCTGTTTGGCTCGGATATAG-ATACCTTAGACTTGGCAATTA 15267
QY 3060 TCAGCAATAGGAATTTATTTTCACAAATCTGAGGCTGGAAATCCAGATCAAGGCTC 3119
DB 15268 TAAACAATAGAAATTCATTCGTGACAGTTGACAGACTGGGAAGTCCAGATCAAGGCG 15327
QY 3120 CAGCAGTTCAGTGTCTGCTGAGTCTGTTGTTCTGCTTCGAGATGCACCTTTTGTGCT 3179
DB 15328 CAGCGAATCTGGTATCTGGTATGCT--CCTGCTTCAAAATGCGGCTCTTGTGCTC 15385
QY 3180 GTTCTCA 3186
DB 15386 ATCTTCA 15392
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RESULT 7

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US-09-804-471A-3
; Sequence 3, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Maxion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 174493
; TYPE: DNA
; ORGANISM: Human
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(174493)
; OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

Query Match          2.6%; Score 82.6; DB 4; Length 174493;
Best Local Similarity 72.2%; Pred. No. 1.1e-14;
Matches 135; Conservative 0; Mismatches 49; Indels 3; Gaps 2;

QY 3000 AATGGTTTGTTCAGTCAGTTTAGGCTGCTATPAAGAGAATATCTTAGAGTGGGTAATCTA 3059
    |||
Db 14097 AAACGTGCATCTGAGTCTGTTTGGGCTGCGATAATAG-ATACCTTAGACTTTGGCAAATTTA 14155

QY 3060 TCAGCAATAGGAATTTATTGTTTCACAATTCGAGGCTGGAAAATCCAAAGATCAAGGCTC 3119
    |||
Db 14156 TAAACAATAGAAATTCATTGCTGACAGTTGTGAAGACTGGGAAGTCCAAGATCAAGGCGC 14215

QY 3120 CAGCAGGTTTCAGTGTCTGCTGAGTGTCTTGTCTTCGATCGAAGATGGCACCTTTTGTGCTGT 3179
    |||
Db 14216 CAGCGAATCTGTTAATCTGTTGATGGCT--CCCTGTCTTCAAAAATGGCGCCTTCTTGCTGC 14273

QY 3180 GTTCTCA 3186
    |||
Db 14274 ATCTTCA 14280

RESULT 8
US-10-238-709-3
; Sequence 3, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001164DIV
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 174493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)...(174493)
; OTHER INFORMATION: n = A,T,C or G
US-10-238-709-3

Query Match          2.6%; Score 82.6; DB 4; Length 174493;
Best Local Similarity 72.2%; Pred. No. 1.1e-14;
Matches 135; Conservative 0; Mismatches 49; Indels 3; Gaps 2;

QY 3000 AATGGTTTGTTCAGTCAGTTTAGGCTGCTATPAAGAGAATATCTTAGAGTGGGTAATCTA 3059
    |||
Db 14097 AAACGTGCATCTGAGTCTGTTTGGGCTGCGATAATAG-ATACCTTAGACTTTGGCAAATTTA 14155

QY 3060 TCAGCAATAGGAATTTATTGTTTCACAATTCGAGGCTGGAAAATCCAAAGATCAAGGCTC 3119
    |||
Db 14156 TAAACAATAGAAATTCATTGCTGACAGTTGTGAAGACTGGGAAGTCCAAGATCAAGGCGC 14215

QY 3120 CAGCAGGTTTCAGTGTCTGCTGAGTGTCTTGTCTTCGATCGAAGATGGCACCTTTTGTGCTGT 3179
    |||
Db 14216 CAGCGAATCTGTTAATCTGTTGATGGCT--CCCTGTCTTCAAAAATGGCGCCTTCTTGCTGC 14273

QY 3180 GTTCTCA 3186
    |||
Db 14274 ATCTTCA 14280

RESULT 9

```

```

US-09-497-855A-40/C
; Sequence 40, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 161652
; TYPE: DNA
; ORGANISM: Homo sapiens,
US-09-497-855A-40

Query Match          2.6%; Score 82.2; DB 4; Length 161652;
Best Local Similarity 69.6%; Pred. No. 1.4e-14;
Matches 126; Conservative 0; Mismatches 53; Indels 2; Gaps 1;

Qy 3007 TGTTTCAGTCAGTTTAGGCTGCTATAGAGAATATCTTAGAGTGGCTAATCTATCAGCAA 3066
Db 13993 TGTCTTGGTCTATTTGTGCTGCTATAACAAATATACCCAAAGCTGGGTAAATTTATATAAAG 13934

Qy 3067 TAGGAATTTATTGTTTCACAAATCTCGAGCTCGAAAAATCCAAAGATCAAGGCTCCAGCAGG 3126
Db 13933 CAGAAATTTAGTCTTCATAGTCTCGAGGCTGGGAAGTCCAAAACCAAGCACTAGCAAG 13874

Qy 3127 TTCAGTCTGCTGAGTG--CTTGTTCTGCTTCGGAAGGCGACCTTTTGTCTGTTCT 3184
Db 13873 TTTTGTGCTGATAGAGGGCCCTGCTCTGCTTCCAAAGATAGTACTTGTGTGCTGATCT 13814

Qy 3185 C 3185
Db 13813 C 13813

RESULT 10
US-09-873-404-3
; Sequence 3, Application US/09873404
; Patent No. 6500656
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THERSOF
; FILE REFERENCE: CL001212-CIP
; CURRENT APPLICATION NUMBER: US/09/873,404
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 3
; LENGTH: 63588
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(63588)
; OTHER INFORMATION: n = A,T,C or G
US-09-873-404-3

```

	Query Match	2.5%	Score 80.8;	DB 4;	Length 63588;
	Best Local Similarity	71.6%;	Pred. No. 2e-14;		
	Matches 106;	Conservative	0;	Mismatches 42;	Indels 0; Gaps 0;
Qy	2999	AAATCGTTTGTTTCAGTTCAGTTAGCTTGGCTATTAAGAGAATATCTTACAGTGGCTAAATCT	3058		
Dh	15658	AAATCTCTGTTTCTCTTATTCCTCAGCAGCTATATACAAATACCAATAAATAGTGGTGGCTT	15717		

QY 3059 ATCAGCATAGCAATTTATTTGTTCAATTTCTGGAGGCTGAAAATCCAGATCAAGCT 3118
Db 15718 ATAAACAGCAGAAATTTATTTCTGCAGTTCTGGAGGCTGGAAGTCAAGATCAAGGTG 15777
QY 3119 CCAGCAGGTTCAAGTCTGCTGCTGAGTGT 3146
Db 15778 CAGGCAGATTCAGTGTCTGCTGAGGTT 15805

RESULT 11

US-09-146-053-4
; Sequence 4, Application US/09146053A
; Patent No. 6393349
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; APPLICANT: Sprinkle, Terry Joe Curtis
; APPLICANT: Venema, Richard C.
; TITLE OF INVENTION: Human Amino-peptidase P Gene
; FILE REFERENCE: MCG103
; CURRENT APPLICATION NUMBER: US/09/146,053A
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/057,854
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 50000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-053-4

Query Match 2.5%; Score 80.4; DB 4; Length 50000;
Best Local Similarity 68.7%; Pred. No. 2.3e-14; Indels 1; Gaps 1;
Matches 125; Conservative 0; Mismatches 56;
QY 3005 TTGTTTCAGTCAGTTAGGCTGCTATAAGAGATATCTTAGAGTGGGTATCTATCAGC 3064
Db 37896 TTTATCTTAGTCCATTGGGGCTGCTATAACAAAGCGCTGCAGACTGCTTGGCTTATAAAC 37955
QY 3065 AATAGGATTTATCTTCAATCTGAGCTGGAATCCAGATCAAGGCTCCAGCA 3124
Db 37956 AGTAGATTTATTTCTTACAGTTCTGGAGCTGGAGTGAAGATCAAGGCACTAGCA 38015
QY 3125 GGTTCAGTGTCTGCTGAGTGTCTGCTTTCGATTCGAAGATGCGACCTTTTGTGTGTCT 3184
Db 38016 GATTGGTGTCCAAACAGGCGCCAGT-TCCTTGTAGATGCGACCTCTCTAGCTGTATCCT 38074
QY 3185 CA 3186
Db 38075 CA 38076

RESULT 12

US-09-497-855A-37
; Sequence 37, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; EARLIER FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 193303
; TYPE: DNA
; ORGANISM: Homo sapiens;

US-09-497-855A-37

Query Match 2.5%; Score 79.2; DB 4; Length 193303;
Best Local Similarity 66.3%; Pred. No. 1.5e-13;
Matches 114; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
QY 3015 TCAGTTTAGGCTGCTATAAGAGATATCTTAGAGTGGGTATCTATCAGCAATAGGAATT 3074
Db 61650 TCAGTCTGCGCACTATAACAAAATACCCAGACTAGGCAATTATAGATAGGAATT 61709
QY 3075 TATTGTTCAATTTCTGGAGGCTGAAAATCCAGATCAAGCTCCAGCAGGTTCAAGTGT 3134
Db 61710 TATTCCATACCAATTTCTGGAGGCTGGAAGTCCAGATCAAGGCACTAGTAGTGTGTGT 61769
QY 3135 CTGCTGAGTGTCTGTTCTGCTTCCAGAGATGCGACCTTTTGTGTGTCTCA 3186
Db 61770 TTGTGACAACTGCTGCTCTGCTTCCAGAGCGGTACCTTGTGTGTCATCTCA 61821

RESULT 13

US-09-497-855A-44
; Sequence 44, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; EARLIER FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 193303
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-09-497-855A-44

Query Match 2.5%; Score 79.2; DB 4; Length 193303;
Best Local Similarity 66.3%; Pred. No. 1.5e-13;
Matches 114; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
QY 3015 TCAGTTTAGGCTGCTATAAGAGATATCTTAGAGTGGGTATCTATCAGCAATAGGAATT 3074
Db 61650 TCAGTCTGCGCACTATAACAAAATACCCAGACTAGGCAATTATAGATAGGAATT 61709
QY 3075 TATTGTTCAATTTCTGGAGGCTGAAAATCCAGATCAAGCTCCAGCAGGTTCAAGTGT 3134
Db 61710 TATTCCATACCAATTTCTGGAGGCTGGAAGTCCAGATCAAGGCACTAGTAGTGTGTGT 61769
QY 3135 CTGCTGAGTGTCTGTTCTGCTTCCAGAGATGCGACCTTTTGTGTGTCTCA 3186
Db 61770 TTGTGACAACTGCTGCTCTGCTTCCAGAGCGGTACCTTGTGTGTCATCTCA 61821

RESULT 14

US-09-671-317-212
; Sequence 212, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; EARLIER FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23

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; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 212
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-500-220 : polymorphic base A or G
; NAME/KEY: misc binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-500-220.misl, potential
; NAME/KEY: misc binding
; LOCATION: 502..521
; OTHER INFORMATION: 12-500-220.mis2, potential complement
; NAME/KEY: primer bind
; LOCATION: 283..303
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer bind
; LOCATION: 711..731
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc binding
; LOCATION: 489..513
; OTHER INFORMATION: 12-500-220 potential probe
; US-09-671-317-212

Query Match 2.5%; Score 79; DB 4; Length 1001;
Best Local Similarity 75.5%; Pred. No. 3.7e-15;
Matches 111; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

Qy 3007 TGTTCAGTCAGTTTAGGCTGCTATAAGA-GAATATCTTAGAGTGGGTAATCTATCAGCA 3065
Db 837 TGTCTTGGTTTGTGGGCTGCTGTACAAAAATACCTTACAGTGGGTGGCTTATAACA 896
Qy 3066 ATAGGAATTTATTGTTTCAACAATTCGGAGGCTGGAAATCCAGATCAAGGCTCCAGCAG 3125
Db 897 ACAGGAATGATTGCTCAGATTCGGAGGCTGGGAAGTTCCAGATCAAGTCACCGGCAG 956
Qy 3126 GTTCAGTGTCTGCTGAGTGTGTCT 3152
Db 957 TTTCGGTGTGGTGAGAGCTTTTGCT 983

RESULT 15
US-09-671-317-458
; Sequence 458, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62 US3 CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm

; SEQ ID NO 458
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-500-217 : insertion CAATA
; NAME/KEY: misc binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-500-217.misl, potential
; NAME/KEY: primer bind
; LOCATION: 286..306
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer bind
; LOCATION: 714..734
; OTHER INFORMATION: downstream amplification primer, complement
; US-09-671-317-458

Query Match 2.5%; Score 79; DB 4; Length 1001;
Best Local Similarity 75.5%; Pred. No. 3.7e-15;
Matches 111; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

Qy 3007 TGTTCAGTCAGTTTAGGCTGCTATAAGA-GAATATCTTAGAGTGGGTAATCTATCAGCA 3065
Db 840 TGTCTTGGTTTGTGGGCTGCTGTACAAAAATACCTTACAGTGGGTGGCTTATAACA 899
Qy 3066 ATAGGAATTTATTGTTTCAACAATTCGGAGGCTGGAAATCCAGATCAAGGCTCCAGCAG 3125
Db 900 ACAGGAATGATTGCTCAGATTCGGAGGCTGGGAAGTTCCAGATCAAGTCACCGGCAG 959
Qy 3126 GTTCAGTGTCTGCTGAGTGTGTCT 3152
Db 960 TTTCGGTGTGGTGAGAGCTTTTGCT 986

Search completed: June 8, 2004, 02:40:40
Job time : 200 secs
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OM protein - protein search, using sw model

Run on: June 7, 2004, 03:03:04 ; Search time 47 Seconds
(without alignments)
2340.498 Million cell updates/sec

Title: US-09-900-448-2

Perfect score: 2185
Sequence: 1 MARVLGAPVALGLWSLWLSL.....NAKALPOPNVTSILGCTH 391

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2185	100.0	391	11	US-09-900-448-2
2	2139.5	97.9	462	11	US-09-900-448-4
3	1556.5	71.2	460	14	US-10-316-353-40
4	1338	61.2	255	15	US-10-182-335-88
5	258	11.8	87	11	US-09-864-408A-1100
6	204	9.3	587	14	US-10-406-209-1
7	202.5	9.3	470	9	US-09-801-196-23
8	202.5	9.3	470	9	US-09-920-455-219
9	202.5	9.3	470	14	US-10-171-111-135
10	202.5	9.3	470	14	US-10-301-822-123
11	202.5	9.3	470	14	US-10-337-832-2
12	202.5	9.3	470	14	US-10-131-985-39
13	202.5	9.3	470	14	US-10-295-027-324
14	202.5	9.3	470	15	US-10-295-027-1243
15	202.5	9.3	470	15	US-10-295-027-1244

16 202.5 9.3 470 15 US-10-409-643-13
17 202.5 9.3 470 16 US-10-188-832-125
18 202.5 9.3 473 9 US-09-925-301-1217
19 199 9.1 519 9 US-09-801-196-30
20 199 9.1 519 14 US-10-131-985-49
21 199 9.1 605 14 US-10-406-209-2
22 199 9.1 605 14 US-10-133-797-5
23 199 9.1 636 12 US-10-425-114-57113
24 196 9.0 464 15 US-10-409-643-21
25 195.5 8.9 477 9 US-09-920-455-260
26 189.5 8.7 475 12 US-10-058-270A-78
27 189.5 8.7 475 15 US-10-295-027-8
28 189.5 8.7 476 9 US-09-801-196-25
29 189.5 8.7 476 12 US-10-211-462-10
30 189.5 8.7 476 14 US-10-021-660-72
31 189.5 8.7 476 14 US-10-131-985-35
32 189.5 8.7 476 16 US-10-188-832-4
33 183.5 8.4 467 9 US-09-801-196-20
34 183.5 8.4 467 10 US-09-759-130B-176
35 183.5 8.4 467 14 US-10-131-985-31
36 182.5 8.4 454 15 US-10-115-479-34
37 181.5 8.3 454 15 US-10-115-479-32
38 181.5 8.3 454 15 US-10-115-479-36
39 181.5 8.3 454 15 US-10-115-479-38
40 181.5 8.3 469 9 US-09-801-196-19
41 181.5 8.3 469 9 US-09-853-386-100
42 181.5 8.3 469 12 US-10-211-462-22
43 181.5 8.3 469 14 US-10-301-822-119
44 181.5 8.3 469 14 US-10-021-660-76
45 181.5 8.3 469 14 US-10-308-279-34

ALIGNMENTS

RESULT 1

US-09-900-448-2

; Sequence 2, Application US/09900448

; Publication No. US20030220488A1

; GENERAL INFORMATION:

; APPLICANT: CECCARDI, Toni et al.

; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: CLO01272

; CURRENT APPLICATION NUMBER: US/09/900,448

; CURRENT FILING DATE: 2001-07-09

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 391

; TYPE: PRT

; ORGANISM: Human

US-09-900-448-2

Query Match 100.0%; Score 2185; DB 11; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.1e-200;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARVLGAPVALGLWSLWLSLAITPLPTSAHGNVAECETKPDPTVTCSCDGSFDTT 60
DB 1 MARVLGAPVALGLWSLWLSLAITPLPTSAHGNVAECETKPDPTVTCSCDGSFDTT 60
QY 61 LDNDGTMLFFKGFYVKSHKWDRELISERWKNFSPVDAAFRQGHNSVFLIKGDKVWYYP 120
DB 61 LDNDGTMLFFKGFYVKSHKWDRELISERWKNFSPVDAAFRQGHNSVFLIKGDKVWYYP 120
QY 121 PEKKEGKGPVKLLQDFPGIPSPDLDAVECHGEQAEVLPFGCHGNCTGHNSTHG 180
DB 121 PEKKEGKGPVKLLQDFPGIPSPDLDAVECHGEQAEVLPFGCHGNCTGHNSTHG 180
QY 181 PEYMRCSHLVLSALTSDNHGATVAPSGTHYWRDLTSDGWHNSWPIAHQWPGQSAYDAA 240

Db 181 PEYWRCSPHVLVSLTSDNKGATVAFSGTHYWLDTSDRGHWSWPIAHQWPQPSAVDAA 240
Qy 241 FSWEEKLYLVQGTQVYVFLTKGGYTLVSGYPKLEKEVGTPHGIIILDSVDAAFICPSSR 300
Db 241 FSWEEKLYLVQGTQVYVFLTKGGYTLVSGYPKLEKEVGTPHGIIILDSVDAAFICPSSR 300
Qy 301 LHIMAGRLWLDLKSQAQATWTLPPHPEKVDGALCMKESLGNPSCSANGPGLYLHGP 360
Db 301 LHIMAGRLWLDLKSQAQATWTLPPHPEKVDGALCMKESLGNPSCSANGPGLYLHGP 360
Qy 361 NLYCYSVDEKLNAAKALPQPNVTSLLGCTH 391
Db 361 NLYCYSVDEKLNAAKALPQPNVTSLLGCTH 391

RESULT 2
US-09-900-448-4
; Sequence 4, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
; APPLICANT: CECARDI, Toni et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001272
; CURRENT APPLICATION NUMBER: US/09/300,448
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Human
US-09-900-448-4

Query Match 97.9%; Score 2139.5; DB 11; Length 462;
Best Local Similarity 84.6%; Pred. No. 3.1e-196;
Matches 391; Conservative 0; Mismatches 0; Indels 71; Gaps 1;

Qy 1 MARVLGAPVALGLWSLWLSLAIAIPLPTSAHGNVAEGE--TKPDPDVTERTCSGDSFPAIT 60
Db 1 MARVLGAPVALGLWSLWLSLAIAIPLPTSAHGNVAEGE--TKPDPDVTERTCSGDSFPAIT 60
Qy 61 LDDNGTMLFFKGEFVWKSMDRELISERWKNFSPVDAAFROGHNSVFLIKGDKVWYYP 120
Db 61 LDDNGTMLFFKGEFVWKSMDRELISERWKNFSPVDAAFROGHNSVFLIKGDKVWYYP 120
Qy 121 PEKKEGYPKLLQDEFFGIPSPHDAAVECHGEQAEGLVFFQ-----GHGRN 169
Db 121 PEKKEGYPKLLQDEFFGIPSPHDAAVECHGEQAEGLVFFQ-----GHGRN 169
Qy 164 -----GHGRN 169
Db 164 -----GHGRN 169
Qy 170 GTGHGNSHTHGPYMRCSPHVLVSLTSDNKGATVAFSGTHYWLDTSDRGHWSWPIAHQ 229
Db 241 GTGHGNSHTHGPYMRCSPHVLVSLTSDNKGATVAFSGTHYWLDTSDRGHWSWPIAHQ 300
Qy 230 WPOGSAVDAAFSWEKLYLVQGTQVYVFLTKGGYTLVSGYPKLEKEVGTPHGIIILDSV 289
Db 301 WPOGSAVDAAFSWEKLYLVQGTQVYVFLTKGGYTLVSGYPKLEKEVGTPHGIIILDSV 360
Qy 290 DAAFTCPGSSRLHIMAGRLWLDLKSQAQATWTLPPHPEKVDGALCMKESLGNPSCSA 349
Db 361 DAAFTCPGSSRLHIMAGRLWLDLKSQAQATWTLPPHPEKVDGALCMKESLGNPSCSA 420
Qy 350 NPGGLYLHGNPNLYCYSDVEKLNAAKALPQPNVTSLLGCTH 391
Db 421 NPGGLYLHGNPNLYCYSDVEKLNAAKALPQPNVTSLLGCTH 462

RESULT 3

US-10-316-253-40
; Sequence 40, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-40

Query Match 71.2%; Score 1556.5; DB 14; Length 460;
Best Local Similarity 63.8%; Pred. No. 2.5e-140;
Matches 296; Conservative 35; Mismatches 54; Indels 79; Gaps 6;

Qy 1 MARVLGAPVALGLWSLWLSLAIAIPLPTSAHGNVAEGE--TKPDPDVTERTCSGDSFPAIT 58
Db 1 MARTVALNAILVLLGLCNSLANVPLP--AAHETVAKGNGTKPDSVDVIEHCSDAWSFDA 58
Qy 59 TTLDDNGTMLFFKGEFVWKSMDRELISERWKNFSPVDAAFROGHNSVFLIKGDKVWY 118
Db 59 TTMDHNGTMLFFKGEFVWKSMDRELISERWKNFSPVDAAFROGHNSVFLIKGDKVWY 117
Qy 119 YPEKKEGYPKLLQDEFFGIPSPHDAAVECHGEQAEGLVFFQGH-----GH-- 167
Db 118 YPEKKEGYPKLLQDEFFGIPSPHDAAVECHGEQAEGLVFFQGH-----GH-- 167
Qy 166 -----GH-- 167
Db 166 -----GH-- 167
Qy 178 ERSWPAVGNCTAALRWLERYYFCQGNKFLRFPVTGEVPPRYPLDARDYFISCPGRGHGK 237
Db 168 -RNGTGHGNSHTHGPYMRCSPHVLVSLTSDNKGATVAFSGTHYWLDTSDRGHWSWPI 226
Qy 238 LRNGTGHGNSHTHGPYMRCSPHVLVSLTSDNKGATVAFSGTHYWLDTSDRGHWSWPI 295
Db 227 AHQWPOGSAVDAAFSWEKLYLVQGTQVYVFLTKGGYTLVSGYPKLEKEVGTPHGIIIL 286
Qy 296 AHQWPOGSAVDAAFSWEKLYLVQGTQVYVFLTKGGYTLVSGYPKLEKEVGTPHGIIIL 355
Db 287 DSVDAAFICPSSRLHIMAGRLWLDLKSQAQATWTLPPHPEKVDGALCMKESLGNPSC 346
Qy 356 DTDAAFICPSSRLHIMAGRLWLDLKSQAQATWTLPPHPEKVDGALCMKESLGNPSC 415
Db 347 CSANGGLYLHGNPNLYCYSDVEKLNAAKALPQPNVTSLLGCT 390
Qy 416 CSSNGPNLFFIHGPNLYCYSDVEKLNAAKALPQPNVTSLLGCT 459
Db 416 CSSNGPNLFFIHGPNLYCYSDVEKLNAAKALPQPNVTSLLGCT 459

RESULT 4
US-10-162-335-88
; Sequence 88, Application US/10162335
; Publication No. US20040009480A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangoili, Bsha A.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda

APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Hjalte, Tord
APPLICANT: Kekuda, Ramesh
APPLICANT: Li, Li
APPLICANT: MacDougall, John R.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Millet, Isabelle
APPLICANT: Padigar, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol E. A.
APPLICANT: Rastelli, Luca
APPLICANT: Shimkets, Richard A.
APPLICANT: Stone, David J.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Voss, Edward Z.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
FILE REFERENCE: 21402-377 B
CURRENT APPLICATION NUMBER: US/10/162,335
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/295,607
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/295,661
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/296,404
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/296,418
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/297,414
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/297,567
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/298,285
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/298,556
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/299,949
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/300,883
PRIOR FILING DATE: 2001-06-26
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 201
SEQ ID NO 88
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
US-10-162-335-88
Query Match 61.2%; Score 1338; DB 15; Length 255;
Best Local Similarity 65.2%; Pred. No. 1e-119;
Matches 255; Conservative 0; Mismatches 0; Indels 136; Gaps 1;
QY 1 MARVLGAPVALGLWSLCLSLAIATPLPTSAHGNVAEGTDPDPVTERCSGDSFDATT 60
DB 1 MARVLGAPVALGLWSLCLSLAIATPLPTSAHGNVAEGTDPDPVTERCSGDSFDATT 60
QY 61 LDNNGTMLFFKGEFVWKSCHKMDRELISRWKNFSPVDAAFRQGENSVFLINGDKVWVYP 120
DB 61 LDNNGTMLFFK----- 71
QY 121 PEKKEKGYPKLLQDEFPPIPSPLDAAVECHRGSCQAEGLVFPQGRHNGTGHGNSHHG 180
DB 72 ----- 71
QY 181 PEYMRCSPLVLSALTSDNHGATYAFSGTHYWRLDTSRDGHSWPIAHQWPGPSAVDAA 240
DB 72 -----GTHYWRLDTSRDGHSWPIAHQWPGPSAVDAA 104
QY 241 FSWEEKLYLVQGTQVYVFLTKGYTLVSGYPKRLEKVGTPHGIIILDSVDAAFICPGSSR 300
DB 105 FSWEEKLYLVQGTQVYVFLTKGYTLVSGYPKRLEKVGTPHGIIILDSVDAAFICPGSSR 164

QY 301 LHIMAGRLWLLDLKSCQAQTWTELPHEKVDGALCMKSLGPNSCSANGPGLYLHGP 360
DB 165 LHIMAGRLWLLDLKSCQAQTWTELPHEKVDGALCMKSLGPNSCSANGPGLYLHGP 224
QY 361 NLYCYSDEVKLNAAKALPOPQNVTSLLGCTH 391
DB 225 NLYCYSDEVKLNAAKALPOPQNVTSLLGCTH 255
RESULT 5
US-09-864-408A-1100
; Sequence 1100, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1100
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
US-09-864-408A-1100

Query Match 11.8%; Score 258; DB 11; Length 87;
Best Local Similarity 86.5%; Pred. No. 8.8e-17;
Matches 45; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 114 DKVWVYPPKKGKGYPKLLQDEFPPIPSPLDAAVECHRGSCQAEGLVFPQGH 165
DB 5 DKVWVYPPKKGKGYPKLLQDEFPPIPSPLDAAVECHRGSCQAEGLVFPQGH 56

RESULT 6
US-10-406-209-1
; Sequence 1, Application US/10406209
; Publication No. US20030170758A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: NOVEL ANTIBODIES, DRUGS CONTAINING THESE ANTIBODIES AND
; TITLE OF INVENTION: METHODS FOR
; TITLE OF INVENTION: SCREENING COMPOUNDS BY USING THESE ANTIBODIES
; FILE REFERENCE: 1241.19
; CURRENT APPLICATION NUMBER: US/10/406,209
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/806,228C
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/JP99/05350
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 10-291501
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 10-291503
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 1
; LENGTH: 587
; TYPE: PRT
; ORGANISM: Mouse
US-10-406-209-1

Query Match 9.3%; Score 204; DB 14; Length 587;
Best Local Similarity 24.4%; Pred. No. 1.8e-10;

Matches 103; Conservative 34; Mismatches 127; Indels 159; Gaps 25;
QY 5 LGAPVALGL-----WSLWSLAIA TEL-----PPTSAHGNVAEGTDPDPV 46
Db 273 VGDPAVAYGLPYEDRVVRWOLYGVRESVPTAQLDTPPEPEPPLLPPPPNNRSTPPQKDV 332
QY 47 TERCSDGWSFDATLDDNGTMLFFKGEFVKSHKWDRELISER-----WKNFP---SP 96
Db 333 PHRCTA--HFDVA--QIRGEAFFKGYKFWLTR--DRHLVSLQPAQHFRWGLPLHLDS 388
QY 97 VDAAF--RQHNSVFLIKGDKVWVYPPPEKKGYPKLLQDEFPGIPSPFLDAAVECHRGECQ 155
Db 389 VDAVVERTSHKIVPFKGDYVWYKDNVVEGYPVPVD--FSLPPGGIDA-----437
QY 156 AEGVLFFQGHGHRNGTGHGNSVTHGPEYMRCSPHLVLSALTSNHCATAPSGTHVWRLD 215
Db 438 ----VPSWAHND-----TTFKQDLWRID 459
QY 216 --TSR--DGHS--WPIAHQWPOGSAVDAAFSWEB--KLYLVQGTQVYVFLTKGGYTLVSG 269
Db 460 DHTFRMDPGYPAQGPL--WRGVPSMLDDAMRWSDCASYFFRG--QYWKVLDGELEAAG 515
QY 270 YPKRLSKE---VTPHGIILSDVDAAFICPGSSRIHIMAGRLWLLDLKSGCAATWELP 326
Db 516 YPQSTARDMLVCGEP-----LADAEDVGGGQ-----SGAQ-----548
QY 327 WPHEKVDG--ALCMKXSLGPNCSGANGPLYLHGPNNLYCVSDVEKLNAAKALPQPQNVTS 385
Db 549 -----DGLAVCS-----CTSDAHL-----ALPSLILLTP 573
QY 386 LL 387
Db 574 LL 575

RESULT 7
US-09-801-196-23
; Sequence 23, Application US/09801196
; Patent No. US20020037827A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Kai
; APPLICANT: Smith, Ryan
; APPLICANT: Pajardo, Mark
; APPLICANT: Moss, Patrick
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
; TITLE OF INVENTION: EXPRESSED IN SKIN CELLS
; FILE REFERENCE: 240083.509
; CURRENT APPLICATION NUMBER: US/09/801.196
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-196-23
Query Match 9.3%; Score 202.5; DB 9; Length 470;
Best Local Similarity 27.3%; Pred. No. 1.9e-10;
Matches 66; Conservative 23; Mismatches 90; Indels 63; Gaps 10;
QY 30 SAHGNVAEGTKPDVTE--RCSGWSFDATLDDNGTMLFFKGEFVW----KSHKWR 83
Db 260 SLYGDPKENQRLPNFDSNPALCDPNLSFDAVTVGN-KIFFKDRFFWLKVSERPKTSV 318
QY 84 ELISERWKNFSPVDAAFR-QGNSVFLIKGDKVWVYPPPEKKGYPKLLQD-EFPGIPS 141
Db 319 NLISLWPTLPSGIEAAVEIARNQVFLKDDKYWLISNLRPEPNPKSIHSGFPNFVK 378
QY 142 PLDAAVECHRGECQAGVLFQGHGHRNGTGHGNSVTHGPEYMRCSPHLVLSALTSNMG 201
Db 379 KIDAAV-----FNPRFY-----391
US-10-171-311-135
; Sequence 135, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersch, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171.311
; CURRENT FILING DATE: 2002-06-12

QY 202 ATYAFSGTHVWRLDTSRD-----GHSWPIAHQWPOGSAVDAAFSWEB--KLYLVQGTQVY 256
Db 392 -TYFVDNQWRYDERRQMDPGYKLLTKFKQGIGPK-IDAVFYSKKNKYVFFQGSNQF 449
QY 257 VF 258
Db 450 EY 451
RESULT 8
US-09-920-455-219
; Sequence 219, Application US/09920455
; Patent No. US20020169647A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF HEAD AND NECK CANCER
; FILE REFERENCE: 210121.540
; CURRENT APPLICATION NUMBER: US/09/920.455
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 275
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 219
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-455-219
Query Match 9.3%; Score 202.5; DB 9; Length 470;
Best Local Similarity 27.3%; Pred. No. 1.9e-10;
Matches 66; Conservative 23; Mismatches 90; Indels 63; Gaps 10;
QY 30 SAHGNVAEGTKPDVTE--RCSGWSFDATLDDNGTMLFFKGEFVW----KSHKWR 83
Db 260 SLYGDPKENQRLPNFDSNPALCDPNLSFDAVTVGN-KIFFKDRFFWLKVSERPKTSV 318
QY 84 ELISERWKNFSPVDAAFR-QGNSVFLIKGDKVWVYPPPEKKGYPKLLQD-EFPGIPS 141
Db 319 NLISLWPTLPSGIEAAVEIARNQVFLKDDKYWLISNLRPEPNPKSIHSGFPNFVK 378
QY 142 PLDAAVECHRGECQAGVLFQGHGHRNGTGHGNSVTHGPEYMRCSPHLVLSALTSNMG 201
Db 379 KIDAAV-----FNPRFY-----391
US-10-171-311-135
; Sequence 135, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersch, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171.311
; CURRENT FILING DATE: 2002-06-12

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; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-135

Query Match          9.3%; Score 202.5; DB 14; Length 470;
Best Local Similarity 27.3%; Pred. No. 1.9e-10;
Matches 66; Conservative 23; Mismatches 90; Indels 63; Gaps 10;

QY 30 SAKGNVAEGTBKDPDPVTE--RCSDCGSPDATTLDNGTMLFFKGEFVW----KSHKWR 83
DB 260 SLYGDPKEHQRLNPNPENSEPALCPNLSFDATTVGN-KLFFPKDRFWMKVSRPKTSV 318
QY 84 ELISERKWNPPSPVDAAFR-QGNSVFLIKGDKVWVYPPKKGKGYPKLLQD-EFGPIPS 141
DB 319 NLTSSWLPTLPSGTEAAVEARNQVFLPKDDKYWLTSNLRPSPNYPKS-HSFGFENFVK 378
QY 142 PLDAAYECHREGCAQAGVLFQFGHENGTHGHGSPYMRCSPHLVLSALTSNDHG 201
DB 379 KIDAAV-----FNRFR----- 391
QY 202 ATYAFSGTHWRLDTSRD----GHSWPIAHQWPGQSAVDAAFSMBEK-LYLVQGTQVY 256
DB 392 -TVFFVDNQWRYDERQXMDPGYPKLTIKNFQIGPK-IDAVFSKNKYVYFQGSNQF 449
QY 257 VF 258
DB 450 EY 451

RESULT 10
US-10-301-822-123
; Sequence 123, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-123

Query Match          9.3%; Score 202.5; DB 14; Length 470;

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Sequence 39, Application US/10131985
Publication No. US20030199440A1
GENERAL INFORMATION:
APPLICANT: Dack, Kevin N
APPLICANT: Davies, Michael J
APPLICANT: Fish, Paul V
APPLICANT: Huggins, Jonathan P
APPLICANT: McIntosh, Fraser S
APPLICANT: McClellan, Nicholas L
TITLE OF INVENTION: Composition
FILE REFERENCE: PCS 10391A
CURRENT APPLICATION NUMBER: US/10/131,985
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: US/09/726,295
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: GB 9930768.8
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-10-131-985-39

Query Match 9.3%; Score 202.5; DB 14; Length 470;
Best Local Similarity 27.3%; Pred. No. 1.9e-10;
Matches 66; Conservative 23; Mismatches 90; Indels 63; Gaps 10;
QY 30 SAHGNVAEGTKPDVDTE--RCSDGWSFDATLDDNGTMLFFKGEFVW----KSHKWR 83
Db 260 SLYGDPKQKRLPNPNSEPALCDPNLSPDAVTVGN-KIFFPKDRFFMLKVSEPKTSV 318
QY 84 ELISERKKNFSPVDAAR-QGNSVPLIKGDKVWVPPKKEKGYPKLLQD-EPPGIPS 141
Db 319 NLISLWPTLPSGTEAAYEARNQVFLPKDKYMLISNLRPEPNYPKSIHSGFPNFK 378
QY 142 PLDAAVECHRGCEQAEGLVFFQGHGHRNGTGHGNSHTEGPEYKRCSPHLVLSALTSN 201
Db 379 KIDAAV-----FNPRFYR----- 391
QY 202 ATYAFSGTHYRLDTSRD----GHSWPIAHQWPGPSAVDAAFSWEK-LYLVOGTQVY 256
Db 392 -TYFFVDNQWRYDERQWMDPGYPKLITKNFQIGPK-IDAVFYSKKNYTYFFQGSNQF 449
QY 257 VF 258
Db 450 EY 451

RESULT 13
US-10-295-027-324
Sequence 324, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666

PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 324
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-324

Query Match 9.3%; Score 202.5; DB 15; Length 470;
Best Local Similarity 27.3%; Pred. No. 1.9e-10;
Matches 66; Conservative 23; Mismatches 90; Indels 63; Gaps 10;
QY 30 SAHGNVAEGTKPDVDTE--RCSDGWSFDATLDDNGTMLFFKGEFVW----KSHKWR 83
Db 260 SLYGDPKQKRLPNPNSEPALCDPNLSPDAVTVGN-KIFFPKDRFFMLKVSEPKTSV 318
QY 84 ELISERKKNFSPVDAAR-QGNSVPLIKGDKVWVPPKKEKGYPKLLQD-EPPGIPS 141
Db 319 NLISLWPTLPSGTEAAYEARNQVFLPKDKYMLISNLRPEPNYPKSIHSGFPNFK 378
QY 142 PLDAAVECHRGCEQAEGLVFFQGHGHRNGTGHGNSHTEGPEYKRCSPHLVLSALTSN 201
Db 379 KIDAAV-----FNPRFYR----- 391
QY 202 ATYAFSGTHYRLDTSRD----GHSWPIAHQWPGPSAVDAAFSWEK-LYLVOGTQVY 256
Db 392 -TYFFVDNQWRYDERQWMDPGYPKLITKNFQIGPK-IDAVFYSKKNYTYFFQGSNQF 449
QY 257 VF 258
Db 450 EY 451

RESULT 14
US-10-295-027-1243
Sequence 1243, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15

; PRIOR APPLICATION NUMBER: US 60/350,666
 ; PRIOR FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/335,394
 ; PRIOR FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: US 60/332,464
 ; PRIOR FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: US 60/334,393
 ; PRIOR FILING DATE: 2001-11-29
 ; PRIOR APPLICATION NUMBER: US 60/340,376
 ; PRIOR FILING DATE: 2001-12-14
 ; PRIOR APPLICATION NUMBER: US 60/347,211
 ; PRIOR FILING DATE: 2002-01-08
 ; PRIOR APPLICATION NUMBER: US 60/347,349
 ; PRIOR FILING DATE: 2002-01-10
 ; PRIOR APPLICATION NUMBER: US 60/355,250
 ; PRIOR FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: US 60/356,714
 ; PRIOR FILING DATE: 2002-02-13
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1386
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1243
 ; LENGTH: 470
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-295-027-1243

Query Match 9.3%; Score 202.5; DB 15; Length 470;
 Best Local Similarity 27.3%; Pred. No. 1.9e-10;
 Matches 66; Conservative 23; Mismatches 90; Indels 63; Gaps 10;
 QY 30 SAGNVAEGTKDDPVTE--RCSGWSFDTATLDDNGTMLFKGEFVW----KSHKWR 83
 DB 260 SLYGDPKRNQRLNPNSSEALCDPLNSFDTATVGN-KIFFFKORFFWLKVSERPKTSV 318
 QY 84 ELISERKKNFPPVDAAFR-QGHSNVFLIKGDKVWVYPPKKEKGYPKLLQD-EFFGIPS 141
 DB 319 NLISLWPTLPSCIEAAYEIEARNQVFLFKDDKYWLISNLRPENYPKSIHSGFGFNFVK 378
 QY 142 PLDAVECHRGECQAGVLPFGQGHNGTGHGNSHTHGPYMRCSPHLVLSALTSNDHG 201
 DB 379 KIDAAV-----FNPRFYR----- 391
 QY 202 ATYAFSGTHYWRDLTSDR-----GWSHPIAHQWPGQPSAVDAAFSWEK-LYLVOGTQVY 256
 DB 392 -TYFFVDNQWRYDRERQWMDPGYKLTNFGIGPK-IDAVFYSKNKYFFFGSSNQF 449
 QY 257 VF 258
 DB 450 EY 451

RESULT 15

US-10-295-027-1244
 ; Sequence 1244, Application US/10295027
 ; Publication No. US20030232350A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Afar, Daniel
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Ginsberg, Wendy M.
 ; APPLICANT: Gish, Kurt C.
 ; APPLICANT: Glynn, Richard
 ; APPLICANT: Hevezi, Peter A.
 ; APPLICANT: Mack, David H.
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Watson, Susan R.
 ; APPLICANT: Eos Biotechnology, Inc.
 ; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 ; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
 ; FILE REFERENCE: 018501-012500US
 ; CURRENT APPLICATION NUMBER: US/10/295,027
 ; CURRENT FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: US 09/663,793

; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: US 60/350,666
 ; PRIOR FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/335,394
 ; PRIOR FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: US 60/332,464
 ; PRIOR FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: US 60/334,393
 ; PRIOR FILING DATE: 2001-11-29
 ; PRIOR APPLICATION NUMBER: US 60/340,376
 ; PRIOR FILING DATE: 2001-12-14
 ; PRIOR APPLICATION NUMBER: US 60/347,211
 ; PRIOR FILING DATE: 2002-01-08
 ; PRIOR APPLICATION NUMBER: US 60/347,349
 ; PRIOR FILING DATE: 2002-01-10
 ; PRIOR APPLICATION NUMBER: US 60/355,250
 ; PRIOR FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: US 60/356,714
 ; PRIOR FILING DATE: 2002-02-13
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1386
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1244
 ; LENGTH: 470
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-295-027-1244

Query Match 9.3%; Score 202.5; DB 15; Length 470;
 Best Local Similarity 27.3%; Pred. No. 1.9e-10;
 Matches 66; Conservative 23; Mismatches 90; Indels 63; Gaps 10;
 QY 30 SAGNVAEGTKDDPVTE--RCSGWSFDTATLDDNGTMLFKGEFVW----KSHKWR 83
 DB 260 SLYGDPKRNQRLNPNSSEALCDPLNSFDTATVGN-KIFFFKORFFWLKVSERPKTSV 318
 QY 84 ELISERKKNFPPVDAAFR-QGHSNVFLIKGDKVWVYPPKKEKGYPKLLQD-EFFGIPS 141
 DB 319 NLISLWPTLPSCIEAAYEIEARNQVFLFKDDKYWLISNLRPENYPKSIHSGFGFNFVK 378
 QY 142 PLDAVECHRGECQAGVLPFGQGHNGTGHGNSHTHGPYMRCSPHLVLSALTSNDHG 201
 DB 379 KIDAAV-----FNPRFYR----- 391
 QY 202 ATYAFSGTHYWRDLTSDR-----GWSHPIAHQWPGQPSAVDAAFSWEK-LYLVOGTQVY 256
 DB 392 -TYFFVDNQWRYDRERQWMDPGYKLTNFGIGPK-IDAVFYSKNKYFFFGSSNQF 449
 QY 257 VF 258
 DB 450 EY 451

Search completed: June 7, 2004, 09:13:02
 Job time : 48 secs

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OM protein - protein search, using sw model

Run on: June 7, 2004, 08:55:29 ; Search time 22 Seconds
(without alignments)
917,534 Million cell updates/sec

Title: US-09-900-448-2

Perfect score: 2185

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Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:**

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	202.5	9.3	470	3	US-08-396-988-2
3	202.5	9.3	470	4	US-09-391-104-26
4	189	9.1	517	4	US-09-391-104-32
5	189.5	8.7	519	3	US-09-211-704A-7
6	189.5	8.7	476	3	US-08-704-711A-21
7	189.5	8.7	476	3	US-08-448-489-14
8	189.5	8.7	476	4	US-09-521-220-21
9	189.5	8.7	476	4	US-09-391-104-22
10	183.5	8.4	444	1	US-09-178-002-2
11	183.5	8.4	467	1	US-09-178-002-4
12	183.5	8.4	467	3	US-09-391-104-24
13	183.5	8.4	468	3	US-08-448-489-13
14	181.5	8.3	469	4	US-09-391-104-23
15	181.5	8.3	492	1	US-07-794-393-4
16	181.5	8.3	492	1	US-08-001-711-4
17	179.5	8.2	488	1	US-07-794-393-2
18	179.5	8.2	488	1	US-08-001-711-2
19	179.5	8.2	488	3	US-08-704-711A-22
20	179.5	8.2	488	4	US-09-521-220-22
21	179.5	8.2	488	4	US-09-391-104-31
22	179.5	8.2	489	3	US-08-448-489-11
23	177	8.1	477	3	US-08-704-711A-20
24	177	8.1	477	3	US-08-448-489-15
25	177	8.1	477	3	US-08-281-313-1
26	177	8.1	477	4	US-09-521-220-20
27	177	8.1	477	4	US-09-391-104-21

28 176.5 8.1 469 3 US-08-704-711A-16 Sequence 16, Appl
29 176.5 8.1 469 3 US-08-448-489-12 Sequence 12, Appl
30 176.5 8.1 469 4 US-09-521-220-16 Sequence 16, Appl
31 176 8.1 471 4 US-09-391-104-25 Sequence 25, Appl
32 176 8.1 471 4 US-08-994-689C-1 Sequence 1, Appl
33 176 8.1 471 4 US-08-994-689C-21 Sequence 21, Appl
34 175 8.0 466 3 US-08-704-711A-17 Sequence 17, Appl
35 175 8.0 466 4 US-09-521-220-17 Sequence 17, Appl
36 172 7.9 564 3 US-09-211-704A-8 Sequence 8, Appl
37 172 7.9 669 3 US-08-704-711A-3 Sequence 3, Appl
38 172 7.9 669 4 US-09-521-220-3 Sequence 3, Appl
39 172 7.9 669 4 US-09-391-104-29 Sequence 29, Appl
40 169.5 7.8 508 4 US-09-391-104-18 Sequence 18, Appl
41 167.5 7.7 411 4 US-09-171-545-3 Sequence 3, Appl
42 167.5 7.7 416 4 US-09-171-545-4 Sequence 4, Appl
43 167.5 7.7 508 4 US-09-171-545-1 Sequence 1, Appl
44 164.5 7.5 324 2 US-08-816-755-2 Sequence 2, Appl
45 164.5 7.5 324 3 US-09-090-673-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-068-392-2
; Sequence 2, Application US/08069392
; Patent No. 6150152
; GENERAL INFORMATION:
; APPLICANT: Shapiro, Steven M.
; TITLE OF INVENTION: Human Macrophage Metalloproteinase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/069,392
; FILING DATE: 19930528
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25275
; REFERENCE/DOCKET NUMBER: 07-24(12406) A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-068-392-2

Query Match 9.3%; Score 202.5; DB 3; Length 470;
Best Local Similarity 27.3%; Pred. No. 2.9e-12;
Matches 66; Conservative 23; Mismatches 90; Indels 63; Gaps 10;
Qy 30 SAHGNVARETGPDPVTE--RCSGWSFDATTLDDNGTGLFFKGEFW---KSHKWR 83
Db 260 SLYGDPKQRLPNPNSEPALCDNLSPDAVTVGN-KIFFKDRFFWLKYSERPKTSV 318
Qy 84 ELTSEKKNFRSPVDAAPR-QGHNSVFLTKGDKVNYPEKKEKGYKLLQD-EFGPIPS 141
Db 319 NLISLWPTLPSGIEAAVEIARNOVFLFKDKYVLSNLRPEPNPKSIHSFGFNPVK 378

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QY 142 PLDAAVECHRGCEQAEGLVFPQGHGHRNGTGHGSHGPEYMRCSPHLVLSALTSNHHG 201
Db 379 KIDAAV-----FNPRFYR----- 391
QY 202 ATYAFSGTHYWLDSRD-----GWHSNPIAHQWPGPSAVDAAFSWEK-LYLVQGTQVY 256
Db 392 -TYFFVDNQWRYDERRQMDPGVFKLITKNFQIGPK-IDAVFYSKNKYFFFGSGNQF 449
QY 257 VF 258
Db 450 EY 451

RESULT 2
US-08-396-988-2
; Sequence 2, Application US/08396988
; Patent No. 6204043
; GENERAL INFORMATION:
; APPLICANT: Shapiro, Steven M.
; TITLE OF INVENTION: Human Macrophage Metalloprotease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/396,988
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/068,392
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25275
; REFERENCE/DOCKET NUMBER: 07-24 (12406)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-396-988-2

Query Match 9.3%; Score 202.5; DB 3; Length 470;
Best Local Similarity 27.3%; Pred. No. 2.9e-12;
Matches 66; Conservative 23; Mismatches 90; Indels 63; Gaps 10;

QY 30 SAHGNVAGETKPDVTS--RCSGWSFDATLLDNGTMLFFKGEFVW----KSHKMDR 83
Db 260 SLYGDPKKNQRLPNPNSEPALCDNLSDAVTTVGN-KIFFKORFFMLKVSRPKTSV 318
QY 84 ELISERWKNFSPVDAAFR-QGHSVFLIKGDKWVYPPKKEKGYKLLQD-EFGIPS 141
Db 319 NLISLWTLPSGIEAAVEIARNQVFLKDKTWLISNLRPEPNYKSHSGFGFPFVK 378
QY 142 PLDAAVECHRGCEQAEGLVFPQGHGHRNGTGHGSHGPEYMRCSPHLVLSALTSNHHG 201
Db 379 KIDAAV-----FNPRFYR----- 391
QY 202 ATYAFSGTHYWLDSRD-----GWHSNPIAHQWPGPSAVDAAFSWEK-LYLVQGTQVY 256
Db 392 -TYFFVDNQWRYDERRQMDPGVFKLITKNFQIGPK-IDAVFYSKNKYFFFGSGNQF 449
QY 257 VF 258
Db 450 EY 451

RESULT 4
US-09-391-104-32
; Sequence 32, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falcuto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; PRIOR FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-26

Query Match 9.3%; Score 202.5; DB 4; Length 470;
Best Local Similarity 27.3%; Pred. No. 2.9e-12;
Matches 66; Conservative 23; Mismatches 90; Indels 63; Gaps 10;

QY 30 SAHGNVAGETKPDVTS--RCSGWSFDATLLDNGTMLFFKGEFVW----KSHKMDR 83
Db 260 SLYGDPKKNQRLPNPNSEPALCDNLSDAVTTVGN-KIFFKORFFMLKVSRPKTSV 318
QY 84 ELISERWKNFSPVDAAFR-QGHSVFLIKGDKWVYPPKKEKGYKLLQD-EFGIPS 141
Db 319 NLISLWTLPSGIEAAVEIARNQVFLKDKTWLISNLRPEPNYKSHSGFGFPFVK 378
QY 142 PLDAAVECHRGCEQAEGLVFPQGHGHRNGTGHGSHGPEYMRCSPHLVLSALTSNHHG 201
Db 379 KIDAAV-----FNPRFYR----- 391
QY 202 ATYAFSGTHYWLDSRD-----GWHSNPIAHQWPGPSAVDAAFSWEK-LYLVQGTQVY 256
Db 392 -TYFFVDNQWRYDERRQMDPGVFKLITKNFQIGPK-IDAVFYSKNKYFFFGSGNQF 449
QY 257 VF 258
Db 450 EY 451

RESULT 4
US-09-391-104-32
; Sequence 32, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falcuto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
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QY 142 PLDAAVECHRGCEQAEGLVFPQGHGHRNGTGHGSHGPEYMRCSPHLVLSALTSNHHG 201
Db 379 KIDAAV-----FNPRFYR----- 391
QY 202 ATYAFSGTHYWLDSRD-----GWHSNPIAHQWPGPSAVDAAFSWEK-LYLVQGTQVY 256
Db 392 -TYFFVDNQWRYDERRQMDPGVFKLITKNFQIGPK-IDAVFYSKNKYFFFGSGNQF 449
QY 257 VF 258
Db 450 EY 451

RESULT 2
US-08-396-988-2
; Sequence 2, Application US/08396988
; Patent No. 6204043
; GENERAL INFORMATION:
; APPLICANT: Shapiro, Steven M.
; TITLE OF INVENTION: Human Macrophage Metalloprotease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/396,988
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/068,392
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25275
; REFERENCE/DOCKET NUMBER: 07-24 (12406)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-396-988-2

Query Match 9.3%; Score 202.5; DB 3; Length 470;
Best Local Similarity 27.3%; Pred. No. 2.9e-12;
Matches 66; Conservative 23; Mismatches 90; Indels 63; Gaps 10;

QY 30 SAHGNVAGETKPDVTS--RCSGWSFDATLLDNGTMLFFKGEFVW----KSHKMDR 83
Db 260 SLYGDPKKNQRLPNPNSEPALCDNLSDAVTTVGN-KIFFKORFFMLKVSRPKTSV 318
QY 84 ELISERWKNFSPVDAAFR-QGHSVFLIKGDKWVYPPKKEKGYKLLQD-EFGIPS 141
Db 319 NLISLWTLPSGIEAAVEIARNQVFLKDKTWLISNLRPEPNYKSHSGFGFPFVK 378
QY 142 PLDAAVECHRGCEQAEGLVFPQGHGHRNGTGHGSHGPEYMRCSPHLVLSALTSNHHG 201
Db 379 KIDAAV-----FNPRFYR----- 391
QY 202 ATYAFSGTHYWLDSRD-----GWHSNPIAHQWPGPSAVDAAFSWEK-LYLVQGTQVY 256
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;; PRIOR APPLICATION NUMBER: US 08/814,394
 ;; PRIOR FILING DATE: 1997-03-11
 ;; NUMBER OF SEQ ID NOS: 35
 ;; SOFTWARE: FastSeq for Windows Version 3.0
 ;; SEQ ID NO 32
 ;; LENGTH: 517
 ;; TYPE: EXT
 ;; ORGANISM: Homo sapiens
 US-09-391-104-32

Query Match 9.1%; Score 199; DB 4; Length 517;
 Best Local Similarity 25.0%; Pred. No. 7,7e-12;
 Matches 80; Conservative 31; Mismatches 123; Indels 86; Gaps 16;
 QY 5 LGAPVALGL-----WSLCWSLAIAIATPL-----PPTSAGNVAEGTETKPPDPVTERCS 51
 DB 188 VGDLRYGLPYEDKVRVWQLYGVRESVSPTAQPEEPILLPEPPDNRRSSAPPRKQVPHRCS 247
 QY 52 DGWSFDATLDDNGTMLFFKGEFVKSHKWDRELISER-----WKNFP---SPVDAAF 101
 DB 248 T--HFDVA--QIRGEAFFKGYFWLTLR--DRHLVSLQPAQWHRFWRGLPLHLSDVDVY 303
 QY 102 -ROGNSVFLIKGDKVWVYPPPEKKEKYPKLLQDFPGIPSPDLAAVECHRGCEQAEGL 160
 DB 304 ERTSDHKIVFFKGDYRWVFKDNVVEGYPRPVSD--FSLPPGGIDAA----- 348
 QY 161 FPOGHGHRNGTGHGNSHTHGPEYMRCSPHLVLSALTSNDHGATYAFSGTHYWRDLT--SRD 219
 DB 349 FSWAHNDR-----TYFFKQQLWRYDDHTRH 374
 QY 220 GWHGWP1-AHQWPGQPSAVDAAFSWEE-KLVIVOGTQVYVFLTKGGYTLVSGYKRLKE 277
 DB 375 MDPGYPASPLWRGVPSLTDAMRWDGASYFFRG-QEYWKVLDGELEVAFCYPOSTARD 433
 QY 278 -----VGTPHGIILDSVDA 292
 DB 434 WLVCQDSQADSGVAAGVDAA 453

RESULT 5
 US-09-211-704A-7

;; Sequence 7, Application US/09211704A
 ;; Patent No. 6271014
 ;; GENERAL INFORMATION:
 ;; APPLICANT: de Saint-Vis, Blandine Marie
 ;; APPLICANT: Fossiez, Francois
 ;; APPLICANT: Caux, Christophe
 ;; APPLICANT: Lebecque, Serge J.E.
 ;; TITLE OF INVENTION: Mammalian Proteinases; Related Reagents
 ;; TITLE OF INVENTION: and Methods
 ;; NUMBER OF SEQUENCES: 10
 ;; CORRESPONDENCE ADDRESS:
 ;; ADDRESS: DNAX Research Institute
 ;; STREET: 901 California Avenue
 ;; CITY: Palo Alto
 ;; STATE: California
 ;; COUNTRY: USA
 ;; ZIP: 94304-1104
 ;; COMPUTER READABLE FORM:
 ;; MEDIUM TYPE: Floppy disk
 ;; COMPUTER: IBM PC compatible
 ;; OPERATING SYSTEM: PC-DOS/MS-DOS
 ;; SOFTWARE: Patent In Release #1.0, Version #1.30
 ;; CURRENT APPLICATION DATA:
 ;; APPLICATION NUMBER: US/09/211,704A
 ;; FILING DATE:
 ;; CLASSIFICATION: 435
 ;; PRIOR APPLICATION DATA:
 ;; APPLICATION NUMBER: US 09/005,263
 ;; FILING DATE: 09-JAN-1998
 ;; ATTORNEY/AGENT INFORMATION:
 ;; NAME: Ching, Edwin P.
 ;; REGISTRATION NUMBER: 34,090

;; REFERENCE/DOCKET NUMBER: SF0781K
 ;; TELECOMMUNICATION INFORMATION:
 ;; TELEPHONE: (650)852-9196
 ;; TELEFAX: (650)496-1200
 ;; INFORMATION FOR SEQ ID NO: 7:
 ;; SEQUENCE CHARACTERISTICS:
 ;; LENGTH: 519 amino acids
 ;; TYPE: amino acid
 ;; STRANDEDNESS: not relevant
 ;; TOPOLOGY: linear
 ;; MOLECULE TYPE: peptide
 US-09-211-704A-7

Query Match 9.1%; Score 199; DB 3; Length 519;
 Best Local Similarity 25.0%; Pred. No. 7,7e-12;
 Matches 80; Conservative 31; Mismatches 123; Indels 86; Gaps 16;
 QY 5 LGAPVALGL-----WSLCWSLAIAIATPL-----PPTSAGNVAEGTETKPPDPVTERCS 51
 DB 190 VGDLRYGLPYEDKVRVWQLYGVRESVSPTAQPEEPILLPEPPDNRRSSAPPRKQVPHRCS 249
 QY 52 DGWSFDATLDDNGTMLFFKGEFVKSHKWDRELISER-----WKNFP---SPVDAAF 101
 DB 250 T--HFDVA--QIRGEAFFKGYFWLTLR--DRHLVSLQPAQWHRFWRGLPLHLSDVDVY 305
 QY 102 -ROGNSVFLIKGDKVWVYPPPEKKEKYPKLLQDFPGIPSPDLAAVECHRGCEQAEGL 160
 DB 306 ERTSDHKIVFFKGDYRWVFKDNVVEGYPRPVSD--FSLPPGGIDAA----- 350
 QY 161 FPOGHGHRNGTGHGNSHTHGPEYMRCSPHLVLSALTSNDHGATYAFSGTHYWRDLT--SRD 219
 DB 351 FSWAHNDR-----TYFFKQQLWRYDDHTRH 376
 QY 220 GWHGWP1-AHQWPGQPSAVDAAFSWEE-KLVIVOGTQVYVFLTKGGYTLVSGYKRLKE 277
 DB 377 MDPGYPASPLWRGVPSLTDAMRWDGASYFFRG-QEYWKVLDGELEVAFCYPOSTARD 435
 QY 278 -----VGTPHGIILDSVDA 292
 DB 436 WLVCQDSQADSGVAAGVDAA 455

RESULT 6

US-08-704-711A-21
 ;; Sequence 21, Application US/08704711A
 ;; Patent No. 6114159
 ;; GENERAL INFORMATION:
 ;; APPLICANT: WILL, Horst
 ;; APPLICANT: HINZMANN, Bernd
 ;; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
 ;; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
 ;; NUMBER OF SEQUENCES: 22
 ;; CORRESPONDENCE ADDRESS:
 ;; ADDRESSEE: Foley & Lardner
 ;; STREET: 3000 K Street, N.W., Suite 500
 ;; CITY: Washington
 ;; STATE: D.C.
 ;; COUNTRY: USA
 ;; ZIP: 20007-5109
 ;; COMPUTER READABLE FORM:
 ;; MEDIUM TYPE: Floppy disk
 ;; COMPUTER: IBM PC compatible
 ;; OPERATING SYSTEM: PC-DOS/MS-DOS
 ;; SOFTWARE: Patent In Release #1.0, Version #1.30
 ;; CURRENT APPLICATION DATA:
 ;; APPLICATION NUMBER: US/08/704,711A
 ;; FILING DATE: 20-NOV-1996
 ;; CLASSIFICATION: 435
 ;; PRIOR APPLICATION DATA:
 ;; APPLICATION NUMBER: WO PCT/DE95/00357
 ;; FILING DATE: 17-MAR-1995
 ;; PRIOR APPLICATION DATA:
 ;; APPLICATION NUMBER: DE 4438838.1

FILING DATE: 21-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-711A-21

Query Match 8.7%; Score 189.5; DB 3; Length 476;
Best Local Similarity 28.4%; Pred. No. 6.6e-11;
Matches 55; Conservative 24; Mismatches 42; Indels 73; Gaps 10;

QY 25 PLPTSAAGNVAGETKPDVTERCSDGWSFDA-TTLDNGTMLFKGFYVWKSHKWR 83
DB 272 PLVPTK---SVPSGSENP-----AKDPALSFDAISTL--RGEYLFKDRYFWRSHWNP 321
QY 84 E-----LISERKNPSPVDAAFR-QGHSVFLIKGDKVWV-----YP 120
DB 322 EPEHLISAFWPSLPSYLDAAVEVNSRDTVFIFKGNFMAIRGNEVQAGYPRGIHTLGFP 381
QY 121 P-----EKK-----EKGYPKLLQDEFPGIPSPPLDAAVE 148
DB 382 PTIRKIDAAVSDKKEKTYFFAADKYWRFDENSQSGFPRLIADDFGVEPKVDAVL- 440
QY 149 CHRGECAQGVLF 162
DB 441 -----QAFGEFFY 448

RESULT 7
US-08-448-489-14
Sequence 14, Application US/08448489
Patent No. 6184022
GENERAL INFORMATION:
APPLICANT: SEIKI, Motoharu
APPLICANT: SATO, Hiroshi
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/08/448,489
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 14
LENGTH: 476
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Known Member of
OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-14

Query Match 8.7%; Score 189.5; DB 3; Length 476;
Best Local Similarity 28.4%; Pred. No. 6.6e-11;
Matches 55; Conservative 24; Mismatches 42; Indels 73; Gaps 10;

QY 25 PLPTSAAGNVAGETKPDVTERCSDGWSFDA-TTLDNGTMLFKGFYVWKSHKWR 83
DB 272 PLVPTK---SVPSGSENP-----AKDPALSFDAISTL--RGEYLFKDRYFWRSHWNP 321
QY 84 E-----LISERKNPSPVDAAFR-QGHSVFLIKGDKVWV-----YP 120

DB 322 EPEHLISAFWPSLPSYLDAAVEVNSRDTVFIFKGNFMAIRGNEVQAGYPRGIHTLGFP 381
QY 121 P-----EKK-----EKGYPKLLQDEFPGIPSPPLDAAVE 148
DB 382 PTIRKIDAAVSDKKEKTYFFAADKYWRFDENSQSGFPRLIADDFGVEPKVDAVL- 440
QY 149 CHRGECAQGVLF 162
DB 441 -----QAFGEFFY 448

RESULT 8
US-09-521-220-21
Sequence 21, Application US/09521220
Patent No. 6399348
GENERAL INFORMATION:
APPLICANT: WILL, Horst
HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/521,220
FILING DATE: 08-Mar-2000
CLASSIFICATION: <Unknown>
21-OCT-1994
17-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/704,711
FILING DATE: <Unknown>
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-521-220-21

Query Match 8.7%; Score 189.5; DB 4; Length 476;
Best Local Similarity 28.4%; Pred. No. 6.6e-11;
Matches 55; Conservative 24; Mismatches 42; Indels 73; Gaps 10;

QY 25 PLPTSAAGNVAGETKPDVTERCSDGWSFDA-TTLDNGTMLFKGFYVWKSHKWR 83
DB 272 PLVPTK---SVPSGSENP-----AKDPALSFDAISTL--RGEYLFKDRYFWRSHWNP 321
QY 84 E-----LISERKNPSPVDAAFR-QGHSVFLIKGDKVWV-----YP 120

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Db 322 EPEFLISAFWPSLSYLDAAVEVNSRDTVFIFKGNFWAIRGNEVQAGYPRGIHTLGGP 381
Qy 121 P-----EKK-----EKGYKLLQDEFFGIPSPDLDAAVE 148
Db 382 PTIRKIDAAVSDKEKKTYFFAADKYWRFDENSQSQMEQGFPLIADDPGVEPKVDVLA- 440
Qy 149 CHRGECAQAGVLFF 162
Db 441 -----QAFGFFYF 448

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RESULT 9

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US-09-391-104-22
; Sequence 22, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; PRIOR FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-22

```

```

Query Match 8.7%; Score 189.5; DB 4; Length 476;
Best Local Similarity 28.4%; Pred. No. 6.6e-11;
Matches 55; Conservative 24; Mismatches 42; Indels 73; Gaps 10;

Qy 25 PLPPTSAGHNVAGETKPDVDVTERCSDGWSFDA-TTLDNGTMLFFKGEFVWKSHKWR 83
Db 272 PLVPTK---SVPSGSEMP-----AKCDPALSFDAISTL--RGEVLFKDYFWRSHWNP 321
Qy 84 E-----IISERKNFSPVDAAFR-QGHSNVLKDKVW-----YP 120
Db 322 EPEFLISAFWPSLSYLDAAVEVNSRDTVFIFKGNFWAIRGNEVQAGYPRGIHTLGGP 381
Qy 121 P-----EKK-----EKGYKLLQDEFFGIPSPDLDAAVE 148
Db 382 PTIRKIDAAVSDKEKKTYFFAADKYWRFDENSQSQMEQGFPLIADDPGVEPKVDVLA- 440
Qy 149 CHRGECAQAGVLFF 162
Db 441 -----QAFGFFYF 448

```

RESULT 10

```

US-09-178-002-2
; Sequence 2, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 444
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
US-09-178-002-2

Query Match 8.4%; Score 183.5; DB 1; Length 444;
Best Local Similarity 24.4%; Pred. No. 2.5e-10;
Matches 60; Conservative 31; Mismatches 80; Indels 75; Gaps 10;

Qy 23 ATPLPPTSAGHNVAGETKPDVDVTERCSDGWSFDA-TTLDNGTMLFFKGEFVWKSH-- 79
Db 242 SNPIQFT-----GPSTFKP-----CDPSLTFFDAITTL--RGEILFFKDYFWRHPQ 286
Qy 80 --KWDRBLISERKNFSPVDAAFRQ-QGHSNVLKDKVWVVPPEKKEKGYPKLLQD-E 135
Db 287 LQRVENNFISLFWPSLTGTAAYEDFDRLFLFKGNQYWALSQYDILQGTPKDISNTG 346
Qy 136 FPGIPSPDLDAAVECHRGECQAGVLFFQGHGHRNGTGHGNSHTHGGPEYMRCSPHLVLSAL 195
Db 347 FSSVQAIDAAV-----FYR----- 361
Qy 196 TSDNHGATYAFSGTHYWRDLTSR---DGMHWNPIAHQWPGQPSAVDAAPSWEEKLYLVQ 252
Db 362 -----SKTYFFVNDQWRYDNQRPMEGPGPKSIGAPPGIESKYDAVFOQEHFFVFS 416
Qy 253 TQVYVF 258
Db 417 PRYAF 422

RESULT 11
US-09-178-002-4
; Sequence 4, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-002-4

```

```

Query Match 8.4%; Score 183.5; DB 1; Length 467;
Best Local Similarity 24.4%; Pred. No. 2.7e-10;
Matches 60; Conservative 31; Mismatches 80; Indels 75; Gaps 10;

Qy 23 ATPLPPTSAGHNVAGETKPDVDVTERCSDGWSFDA-TTLDNGTMLFFKGEFVWKSH-- 79
Db 265 SNPIQFT-----GPSTFKP-----CDPSLTFFDAITTL--RGEILFFKDYFWRHPQ 309
Qy 80 --KWDRBLISERKNFSPVDAAFRQ-QGHSNVLKDKVWVVPPEKKEKGYPKLLQD-E 135
Db 310 LQRVENNFISLFWPSLTGTAAYEDFDRLFLFKGNQYWALSQYDILQGTPKDISNYG 369
Qy 136 FPGIPSPDLDAAVECHRGECQAGVLFFQGHGHRNGTGHGNSHTHGGPEYMRCSPHLVLSAL 195
Db 370 FSSVQAIDAAV-----FYR----- 384
Qy 196 TSDNHGATYAFSGTHYWRDLTSR---DGMHWNPIAHQWPGQPSAVDAAPSWEEKLYLVQ 252
Db 385 -----SKTYFFVNDQWRYDNQRPMEGPGPKSIGAPPGIESKYDAVFOQEHFFVFS 439
Qy 253 TQVYVF 258
Db 440 PRYAF 445

RESULT 12
US-09-391-104-24

```

; Sequence 24, Application US/09391104

; Patent No. 6399371

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Faiduto, Michael T.

; APPLICANT: Magnuson, Scott R.

; APPLICANT: Morgan, Douglas W.

; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE.

; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS

; TITLE OF INVENTION: OF USING SAME

; FILE REFERENCE: 6073.US.P1

; CURRENT APPLICATION NUMBER: US/09/391,104

; CURRENT FILING DATE: 1999-08-07

; PRIOR APPLICATION NUMBER: US 08/814,394

; PRIOR FILING DATE: 1997-03-11

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 24

; LENGTH: 467

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-391-104-24

Query Match 8.4%; Score 183.5; DB 4; Length 467;

Best Local Similarity 24.4%; Pred. No. 2.7e-10;

Matches 60; Conservative 31; Mismatches 80; Indels 75; Gaps 10;

QY 23 ATPLPPTSAHGNVAEGTKPDVTERCSDGWSFDA-TTLDNGTMLFFKGFVWKSH-- 79

DB 265 SNPQPT-----GPTPKP-----CDPSLTDAITTL--RGEILFFKDRYFWRHPQ 309

QY 80 --KWDRELISBRWNKFPSPVDAAFQ--GHNSVFLIKGDKVWVYPPPEKKEGYPKLLQD-E 135

DB 310 LQVEMNFISLFWPSLPTGICAAVEDFDRLIIFLKGNQYWALSGYDILQGYPKDISNYG 369

QY 136 PPGIPSPLDAAVECHRGCEQAGVLFQGHGRNGTGHGNSHHGPEYMCSPHLVLSAL 195

DB 370 FESSVQIDAAY-----FYR----- 384

QY 196 TSDNHGATYAFSGTHYWRDLTSR---DGHWSWPIAHQWPGSPSAVDAAFSWEKLYLVQ 252

DB 385 -----SKTYFFVNDQFWRYDNQRFMEPGYPKSIGAPPGIESKVDVAFQOEHHFVFSG 439

QY 253 TQVYVF 258

DB 440 PRYVAP 445

RESULT 13

US-08-448-489-13

; Sequence 13, Application US/08448489

; Patent No. 6184022

; GENERAL INFORMATION:

; APPLICANT: SEIKI, Motoharu

; APPLICANT: SATO, Hiroshi

; APPLICANT: SHINAGAWA, Akira

; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR

; FILE REFERENCE: 55-290P

; CURRENT APPLICATION NUMBER: US/08/448,489

; CURRENT FILING DATE: 1995-06-07

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 13

; LENGTH: 468

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: X = UNKNOWN

; OTHER INFORMATION: Description of Unknown Organism: Known Member of

; OTHER INFORMATION: Matrix Metalloproteinase Family

; US-08-448-489-13

Query Match

Best Local Similarity 8.4%; Score 183.5; DB 3; Length 468;

Matches 60; Conservative 31; Mismatches 80; Indels 75; Gaps 10;

QY 23 ATPLPPTSAHGNVAEGTKPDVTERCSDGWSFDA-TTLDNGTMLFFKGFVWKSH-- 79

DB 265 SNPQPT-----GPTPKP-----CDPSLTDAITTL--RGEILFFKDRYFWRHPQ 309

QY 80 --KWDRELISBRWNKFPSPVDAAFQ--GHNSVFLIKGDKVWVYPPPEKKEGYPKLLQD-E 135

DB 310 LQVEMNFISLFWPSLPTGICAAVEDFDRLIIFLKGNQYWALSGYDILQGYPKDISNYG 369

QY 136 PPGIPSPLDAAVECHRGCEQAGVLFQGHGRNGTGHGNSHHGPEYMCSPHLVLSAL 195

DB 370 FESSVQIDAAY-----FYR----- 384

QY 196 TSDNHGATYAFSGTHYWRDLTSR---DGHWSWPIAHQWPGSPSAVDAAFSWEKLYLVQ 252

DB 385 -----SKTYFFVNDQFWRYDNQRFMEPGYPKSIGAPPGIESKVDVAFQOEHHFVFSG 439

QY 253 TQVYVF 258

DB 440 PRYVAP 445

RESULT 14

US-09-391-104-23

; Sequence 23, Application US/09391104

; Patent No. 6399371

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Faiduto, Michael T.

; APPLICANT: Magnuson, Scott R.

; APPLICANT: Morgan, Douglas W.

; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE.

; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS

; FILE REFERENCE: 6073.US.P1

; CURRENT APPLICATION NUMBER: US/09/391,104

; CURRENT FILING DATE: 1999-09-07

; PRIOR APPLICATION NUMBER: US 08/814,394

; PRIOR FILING DATE: 1997-03-11

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 23

; LENGTH: 469

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-391-104-23

Query Match

Best Local Similarity 8.3%; Score 181.5; DB 4; Length 469;

Matches 59; Conservative 26; Mismatches 82; Indels 57; Gaps 8;

QY 44 PDVTERCSDGWSFDA-TTLDNGTMLFFKGFVWKSHKWDREL----ISRWKNFSPVD 98

DB 272 PQTPEKACDSKLTDAITTI--RGEVMPFKDRFYMRTPFPYPEVELNFIISVFWPLQPNLE 329

QY 99 AAFR--QGHSVFLIKGDKVWVYPPPEKKEGYPKLLQDEFPPIPSPLDAAVECHRGCEQAE 157

DB 330 AAYEPADREDEVRFFGKNYNAVQONVHGYPKDIYSSP-GFP----- 371

QY 158 GVLFFQGHGRNGTGHGNSHHGPEYMCSPHLVLSALTSDNHGATYAFSGTHYWRDL-- 215

DB 372 -----RTVKH-IDAALSEENTGKTFFVANKYWRDEY 403

QY 216 -TSRDGHSWPIAHQWPGSPSAVDAAFSWEKLYLVQGTQVYVF 258

DB 404 KRSKDPGYPKMIANDPFGIGHKVDVAVFMKDGFFFFHGTQYKF 447

RESULT 15

US-07-794-393-4

; Sequence 4, Application US/07794393
; Patent No. 5236844
; GENERAL INFORMATION:
; APPLICANT: CHAMBERON, PIERRE
; APPLICANT: BASSET, PAUL
; APPLICANT: BELLOCO, JEAN-PIERRE
; TITLE OF INVENTION: ANALYTICAL MARKERS FOR MALIGNANT BREAST
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07794,393
; FILING DATE: 19911121
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9025326.1
; FILING DATE: 21-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1383.0040000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 492 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-794-393-4

Query Match 8.3%; Score 181.5; DB 1; Length 492;
Best Local Similarity 25.2%; Pred. No. 4.7e-10;
Matches 69; Conservative 26; Mismatches 86; Indels 93; Gaps 13;
QY 24 TPLPPTSAH-----GNVAGETKPDVPTERCSDGWSFDATLLDDNGTMLPFKGRFVWKS 78
DE 270 SPAPTLSSQAGTDNTEIALLEPETPPDYCET-----SFDAYS-TIRGELFFFKAGFVWRL 323
QY 79 HKWDR-----LISRMKNFSPVDAAPROGHNSVFLIKGDKVWVYPPKKKGYPKLLQ 133
DB 324 RSGRLQPGYPALASRHHWGLSPVDAAFEDAQGOIWFQGAQVWYDGEKPVLGPAFLSK 383
QY 134 DEFPGLPSPLDAVVECHRGBCQAEGLVLPFGQGHNGTGHGNSHTHGPEYMRCSPLVLS 193
DB 384 LGLQG--SPVHAALV-----WGPE-----400
QY 194 ALTDNNGATVAFSGTHYWRLLD--TSR-DGWHSNPIAHQ---NPQGPSAVDAAFSWEKL 247
DB 401 -----KNKLYFFRGDYYRFRHPTQVDN-----PVPRSTDMRGVSEIDAAF-----444
QY 248 YLVQGTQVYVFLTKG-----GYTLVSGYPK 272
DB 445 ---QDAEGYAYFLRGHLYKFKDPVKVKVLEGFPR 475

Search completed: June 7, 2004, 09:08:12
Job time : 23 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2004, 05:38:24 ; Search time 535 Seconds
(without alignments)
3334.094 Million cell updates/sec

Title: US-09-900-448-2

Perfect score: 2185

Sequence: 1 MARVLGAPVALGLWSLWSL.....NAKALPQNVVTLGGCTH 391

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-D=Published Applications NA -QWTF=fastcap -SUPTFX=p2n.rnpb -MINMATCH=0.1
-LOQ2CL=0 -LOQEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS-human40 cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFM=pc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09900448 -CGEN 1 1 221 @runat_07062004_094659_20503
-NCFU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq.*
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7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq.*
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10: /cgn2_6/prodata/2/pubpna/US09A_PUBCOMB.seq.*
11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq.*
18: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2185	391	391	391	391

Alignment Scores:	1.58e-230	Length:	3186
Pred. No.:	2185.00	Matches:	391

ALIGNMENTS

RESULT 1

US-09-900-448-1
; Sequence 1, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
; APPLICANT: CECARDI, Toni et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO01272
; CURRENT APPLICATION NUMBER: US/09/900,448
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3186
; TYPE: DNA
; ORGANISM: Human
; US-09-900-448-1

Alignment Scores:	1.58e-230	Length:	3186
Pred. No.:	2185.00	Matches:	391

Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-09-900-448-2 (1-391) x US-09-900-448-1 (1-3186)

QY 1 MetAlaArgValLeuGlyAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
 DB 15 ATGGCTAGGCTACTGGGAGCACCGGTGCTGCTGGGCTTGTGGAGCTATGCTGCTCTG 74
 QY 21 AlAlaLeaThrProLeuProThrSerAlaHisGlyAsnValAlaGluGlyLeuThr 40
 DB 75 GCAATGGCCACCCCTCTCTCCGACTAGTGGCCATGGGATGTGTGAGGCGAGACC 134
 QY 41 LysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThr 60
 DB 135 AAGCCAGACCCAGAGCTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGATGCTTACCA 194
 QY 61 LeuAspAspAsnGlyThrMetLeuPhePheLeuGlyGluPheValTrpLysSerHisLys 80
 DB 195 CTGGATGACAAATGGAACCACTGCTGTTTAAAGGGGAGTTTGTGTGAAGAGTCACAAA 254
 QY 81 TrpAspArgGluLeuLeuSerGluArgTrpLysAsnPheProSerProValAspAlaAla 100
 DB 255 TGGGACCGGGAGTTAATCTCAGAGAGATGGAAGAAATTTCCCGACGCTGTGGATGCCA 314
 QY 101 PheArgGlnGlyHisAsnSerValPheLeuLeuLysGlyAspLysValTrpValTrpPro 120
 DB 315 TTCCGTCAAGGTACACACAGTGTCTTCTGATCAAGGGGGACAAAGTCTGGGTATACCT 374
 QY 121 ProGluLysGlyGluGlyGlyTrpProLysLeuLeuGlnAspGluPheProGlyLeuPro 140
 DB 375 CTGGAAGAAGAGGAGAAAGGATACCAAGTTGTCTCCAGAGAAATTTCTGGGAATCCCA 434
 QY 141 SerProLeuAspAlaAlaValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeu 160
 DB 435 TCCCACTGGATGAGCTGTGGAATGTCCAGCTGGAGAAATGTCAAGCTGAAGGCTCTC 494
 QY 161 PhePheGlnGlyHisGlyHisArgAsnGlyThrGlyHisGlyAsnSerThrHisGly 180
 DB 495 TTCCTTCCAGGCGCATGGGACACAGGAATGGGATGGGCTGCCATGGGAACAGTACCCACATGGC 554
 QY 181 ProGluTrpMetArgCysSerProHisLeuValLeuSerAlaLeuThrSerAspAsnHis 200
 DB 555 CCTGAGTATATGCGCTGTAGCCCACTACTGTCTGTCTGCACTGACGTCTGACACCAT 614
 QY 201 GlyAlaThrThrAlaPheSerGlyThrHisTrpArgLeuAspThrSerArgAspGly 220
 DB 615 GGTGCCACCTATGCTTCACTGGGACCCCACTACTGGGCTCTGGACACCCAGCGGGATGGC 674
 QY 221 TrpHisSerTrpProLeuAlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAla 240
 DB 675 TGGCATAGCTGGCCCATTTGCTCATCAGTGGGCCCGCCAGGGTCTTCAGCAGTGGATGCTGCC 734
 QY 241 PheSerTrpGluGluLysLeuTrpLeuValGlnGlyThrGlnValTrpValPheLeuThr 260
 DB 735 TTTTCTCGGAAGAAAAAATCTATCTGCTCCAGGGCACCCAGGTATATGCTTCTCTGACA 794
 QY 261 LysGlyGlyTrpThrLeuValSerGlyTrpProLysArgLeuGluLysGluValGlyThr 280
 DB 795 AAGGGAGGCTATACCTAGTAGCGGTATCCGAGCGGCTGGGAGAGGAGTGGGAGC 854
 QY 281 ProHisGlyTrpLeuAspSerValAspAlaPheLeuCysProGlySerSerArg 300
 DB 855 CCTCAGGAGTATATCTGGACTCTGTGATGGGCTTTATCTCCCTGGGTCTTCTCGG 914
 QY 301 LeuHisIleMetAlaGlyArgLeuTrpTrpLeuAspLeuLysSerGlyValAlaGlnAla 320
 DB 915 CTCCATATCATGGCAGGAGCGGCTGTGTGGCTGGACCTGAGCTGAGTCAAGGAGCCAGCC 974
 QY 321 ThrTrpThrGluLeuProTrpProHisGluLysValAspGlyAlaLeuCysMetGluLys 340

DB 975 ACCTGGACAGAGCTTCTTGGCCCCCANGAGAGAGGTAGACGGAGCCTTGTGTATGGAAG 1034
 QY 341 SerLeuGlyProAsnSerCysSerAlaAsnGlyProGlyLeuTrpLeuLeuHisGlyPro 360
 DB 1035 TCCCTTGGCCCTAACTCAATGTTCCGCAATGTTCCCGGCTTGTACTCTCATCATGTTCC 1094
 QY 361 AsnLeuTrpCysTrpSerAspValGlnLysLeuAsnAlaAlaLysAlaLeuProGlnPro 380
 DB 1095 AATTTGTACTGTACTAGTGTAGTGTGAGAAACTGAATGAGCCCAAGCCCTTCCGCAACC 1154
 QY 381 GlnAsnValThrSerLeuLeuGlyCysThrHis 391
 DB 1155 CAGAATGTGACCACTCTCTCGGGCTGCACTCAC 1187

RESULT 2

US-10-125-237-19
 ; Sequence 19, Application US/10125237
 ; Publication No. US20030022329A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Drmanac, Radoje T.
 ; TITLE OF INVENTION: NO. US20030022329A1el Nucleic Acids and
 ; FILE REFERENCE: 79ICPZADIV
 ; CURRENT APPLICATION NUMBER: US/10/125,237
 ; CURRENT FILING DATE: 2002-04-17
 ; PRIOR APPLICATION NUMBER: 09/668,317
 ; PRIOR FILING DATE: 2000-09-22
 ; PRIOR APPLICATION NUMBER: 09/552,929
 ; PRIOR FILING DATE: 2000-04-18
 ; NUMBER OF SEQ ID NOS: 91
 ; SOFTWARE: pt_FL_genes Version 2.0
 ; SEQ ID NO 19
 ; LENGTH: 1631
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (71)..(1459)
 ; US-10-125-237-19

Alignment Scores:
 Pred. No.: 7,01e-226 Length: 1631
 Score: 2139.50 Matches: 391
 Percent Similarity: 84.63% Conservative: 0
 Best Local Similarity: 84.63% Mismatches: 0
 Query Match: 97.92% Indels: 71
 DB: 15 Gaps: 1

US-09-900-448-2 (1-391) x US-10-125-237-19 (1-1631)

QY 1 MetAlaArgValLeuGlyAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
 DB 71 ATGGCTAGGCTACTGGGAGCACCGGTGCTGCTGGGTTGTGGAGCTTATGCTGCTCTG 130
 QY 21 AlAlaLeaThrProLeuProThrSerAlaHisGlyAsnValAlaGluGlyLeuThr 40
 DB 131 GCAATGGCCACCCCTCTCTCCGACTAGTGGCCATGGGATGTGTGAGGCGAGACC 190
 QY 41 LysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThr 60
 DB 191 AAGCCAGACCCAGAGCTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGATGCTACACC 250
 QY 61 LeuAspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHisLys 80

Db	251	CTGAGTGA	CAATGGGA	CCATCGTGT	TTTAAAGGGG	AGTTGT	GTGTGGGA	AGAGTGCACAAA	311			
Qy	81	TrpAspArg	GluLeu	IleSer	GluArg	TrpIys	AsnPhe	ProSer	ProVal	AspAla	ala	100
Db	311	TGGGAC	CGGGAG	TTAATCT	CACAGAGAT	GGAAGAA	TTCC	CCAGCCCT	GTGTGGAT	CTGCA	370	
Qy	101	PheArg	GlnGln	IleHis	AsnSer	ValPhe	LeuIle	IysGly	AspIys	ValTrp	ValTrp	120
Db	371	TTCCGT	CAAGGT	CAAA	CAGTGT	CTTTCT	GATCAG	GGGACA	CAAGTCT	TGGGTA	TACCC	430
Qy	121	ProGlu	LysGly	SerGly	TrpPro	LysLeu	IleGlu	AspGlu	PhePro	GlyIle	Pro	140
Db	431	CCGTGAAA	AGAGAG	AAAGGAT	ACCAAG	TTCT	CCAGAT	GATAT	TTCT	TGAT	TCCCA	490
Qy	141	SerPro	LeuAsp	AlaAla	ValGln	CysHis	ArgGly	GlyCys	GlnAla	chlGly	ValLeu	160
Db	491	TCCCACT	TGGAT	GCAGCT	GTGGAAT	GTAC	CGTGGAA	TGTCA	AGCTGAA	GGCTGC	TCC	550
Qy	161	PhePhe	Gln									163
Db	551	TTCTT	CCAAGG	TGAC	CGGAGT	TGGT	TTCT	TGGGAC	TTGGCT	ACGGGA	ACCATGAAG	610
Qy	163											163
Db	611	TCCTGG	CCAGCT	TTGGGA	ACTGCT	CTCTG	CCCTGAGAT	GGCTGGG	CCGCTACT	ACTG	TC	670
Qy	163											163
Db	671	TTCCAG	GGTAA	CCAAT	TCCTG	CGCTT	CGAC	CCCTGT	CAGGGG	AGAGTG	CTCC	730
Qy	164											169
Db	731	CGCGGG	ATGTC	CGAG	ACTACT	TCAT	GCCTG	CCCTGG	CCAGAG	GCCTG	GA	790
Qy	170	GlyThr	GlyHis	GlyAsn	SerThr	HisHis	GlyPro	GluTyr	MetArg	CysSer	ProHis	189
Db	791	GGGAT	GTGG	CCAT	TGGAA	CAGTAC	CCAC	CATGG	CCCTGAGT	TATATG	CTGTAG	850
Qy	190	LeuVal	LeuSer	AlaLeu	ThrSer	AspAsn	HisGly	ValAla	ThrTyr	AlaPhe	SerGly	209
Db	851	CTAGT	CTTGT	CTGAC	TGAC	GTCT	GAAC	CAATG	GTGCC	ACTATG	CCCTCAGTGG	910
Qy	210	HisTyr	TrpArg	LeuAsp	ThrSer	ArgAsp	GlyTrp	HisSer	TrpPro	IleAla	HisGln	229
Db	911	CNACT	ACTGG	CGCT	TGGAC	CAC	CAG	CGGGAT	TGGCTGG	CATAGT	TGGCCCAT	970
Qy	230	TrpPro	GlnGly	ProSer	AlaVal	AspAla	AlaPhe	SerTrp	GluGlu	LysLeu	TyrLeu	249
Db	971	TGGCCCC	AGGGT	CTCT	CAGCAG	TGGAT	CTGCTCT	TTTCT	TGGGA	AGAAACT	CTATCTG	1030
Qy	250	ValGln	GlyThr	GlnVal	TyrVal	PheLeu	ThrLys	GlyGly	TyrThr	LeuVal	SerGly	269
Db	1031	GTCC	AGGAC	CCCA	AGGTAT	TATG	CTCT	GCACAA	AGGAGG	GTATAC	CCCTAGTAA	1090
Qy	270	TyrPro	LysArg	LeuGlu	LysGlu	ValGly	ThrPro	HisGly	IleLeu	AspSer	Val	289
Db	1091	TATCC	GAAG	CGCT	TGGAG	AGAGT	TCGG	ACCCCT	CATGG	AGTATAT	CTTCTG	1150
Qy	290	AspAla	AlaPhe	IleCys	ProGly	SerArg	LeuHis	IleMet	AlaGly	ArgArg	Leu	309
Db	1151	GATCG	GGCTTT	ATCT	CTGCC	CTGG	GTCTCT	TCGG	CTCCAT	TATCAT	GGCAGAG	1210
Qy	310	TrpTrp	LeuAsp	LeuLys	SerGly	ValAla	GlnAla	ThrTyr	ThrGlu	LeuPro	TrpPro	329
Db	1211	TGTT	GGCTGG	ACCT	TGAAGT	CAGGAG	CCCA	AGCCAC	GTGG	CACAG	AGCTT	1270
Qy	330	GluLys	ValAsp	GlyAla	LeuCys	MetGlu	LysSer	LeuGly	ProAsn	SerCys	SerAla	349
Db	1271	GAGA	AGGTAG	ACGAG	CCCT	TGTGTAT	GGA	AAAGT	CCCTT	GGCCCT	TAATCAT	1330
Qy	350	AsnGly	ProGly	LeuTyr	LeuIle	HisGly	ProAsn	LeuTyr	CysTyr	SerAsp	ValGlu	369

```

Db      1331  AATGGTCCCGGCTTGACTCATCAATGAGTGGTCCCAATTTGTACTGTGCTACATGATGTGGAG 1399
Qy      370   LysLeuAsnAlaAlaLysAlaLeuProGlnProGlnAsnValThrSerLeuLeuGlyCys 389
Db      1391  AAACCTGAATGCAGCCAGGCGCCCTTCGCAACCCAGAAATGTGACCAGTCTCTCTGGGCTGC 1450
Qy      390   ThrHis 391
Db      1451  ACTCAC 1456

RESULT 3
US-10-105-891-19
: Sequence 19, Application US/10105891
: Publication No. US20030073099A1
: GENERAL INFORMATION:
: APPLICANT: Tang, Y. Tom
: APPLICANT: Liu, Chenghua
: APPLICANT: Zhou, Ping
: APPLICANT: Asundi, Vinod
: APPLICANT: Ren, Feiyan
: APPLICANT: Zhao, Qing A.
: APPLICANT: Xue, Aidong J.
: APPLICANT: Zhang, Jie
: APPLICANT: Wehrman, Tom
: APPLICANT: Wang, Jian-Rui
: APPLICANT: Drmanac, Radjko T.
: TITLE OF INVENTION: No. US20030073099A1el Nucleic Acids and
: FILE REFERENCE: 791CIP2A
: CURRENT APPLICATION NUMBER: US/10/105,891
: PRIOR FILING DATE: 2002-03-25
: PRIOR APPLICATION NUMBER: 09/668,317
: PRIOR FILING DATE: 2000-09-22
: PRIOR APPLICATION NUMBER: 09/552,929
: PRIOR FILING DATE: 2000-04-18
: NUMBER OF SEQ ID NOS: 91
: SOFTWARE: pt_FL_genes Version 2.0
: SEQ ID NO 19
: LENGTH: 1631
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (71)..(1459)
US-10-105-891-19

Alignment Scores:
Pred. No.: 7,01e-226 Length: 1631
Score: 2139.50 Matches: 391
Percent Similarity: 84.63% Conservatives: 0
Best Local Similarity: 84.63% Mismatches: 0
Query Match: 97.92% Indels: 71
DB: 15 Gaps: 1

US-09-900-448-2 (1-391) x US-10-105-891-19 (1-1631)

Qy      1   MetaAargValLeuGlyAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
Db      71   ATGCTTAGGTACTGGAGCACCCGTTGACTGGGTTGTGGAGCCCTATGCTGGTCTCTG 130
Qy      21   AlailAlaThrProLeuProProThrSerAlaHisGlyAsnValalalaGluGlyGluThr 40
Db      131  GCCATTGCCACCCTCTCTCTCGACTAGTGCCTGAGGAATGTTGCTGAAGCGAGACC 190
Qy      41   LysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThr 60
Db      191  AAGCCAGACCCAGACCTGACTGAACGCTCTCAGATGGCTGGAGCTTTGATGCTACCACC 250
Qy      61   LeuAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHisLys 80
Db      251  CTGATGACAAATGGAAACCATGCTGTTTTTTAAAGGGGAGTTTGTGTGGAAGAGTGCACAA 310
Qy      81   TrpAspArgGluLeuIleSerGluArgTrpLysAsnPheProSerProValAspAlaAla 100

```


Db 311 TGGACCGGAGTAAATCTCAGAGATGAAGAATTTCCTCCAGCCCTGTGGATGCTGCA 370
Qy 101 PheArgGlnGlyHisAsnSerValPheLeuIleGlyAspIleValTrpValTrpPro 120
Db 371 TTCCTGCAAGGTCAACACAGTGTCTTCTGATCAAGGGGCAAGAATCTGGTATACCT 430
Qy 121 ProGluIleGlyLeuIleGlyProIleGlyLeuIleGlyLeuIleGlyLeuIlePro 140
Db 431 CCTGAAAGAGGAGGAGGATACCCAAAGTGTCTCCAGATGAATTTCTCGAATCCCA 490
Qy 141 SerProLeuAspAlaAlaValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeu 160
Db 491 TCCCATCTGGATGCGCTGTGGATGTCTACCGTGAAGATGTCAAGCTGAAGGGTCTTC 550
Qy 161 PhePheGln 163
Db 551 TTCTTCAAGGTGACCGAGTGGTCTTGGGACTTGGCTACGGGAACCATGAAGAGCGT 610
Qy 163 163
Db 611 TCCTGGCCAGCTGTGGAACTGCTCTCTGCTGCTGAGATGGCTGGCGCGCTACTACTGC 670
Qy 163 163
Db 671 TTCCAGGTAACCAATTCCTGCGCTTGCACCTGTCTCAGGGGAGAGTGCCTCCAGGTAC 730
Qy 164 164
Db 731 CCGCGGATGTCGAGACTACTTCATGCCCTGCCCTGGCAGAGGTCCTCCAGGAGT 790
Qy 170 GlyThrGlyHisGlyAsnSerHisHisGlyProGluIleMetArgCysSerProHis 189
Db 791 GGGACTGGCCATGGGAACAGTACCCACCATGCCCTGAGTATATGCGCTGTAGCCACAT 850
Qy 190 LeuValLeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPheSerGlyThr 209
Db 851 CTAGTCTTGTCTGCACTGACCTCTGACACCATGCTGCCACCTATGCTTCAGTGGGACC 910
Qy 210 HisTyrTrpArgLeuAspThrSerArgAspGlyTrpHisSerTrpProIleAlaHisGln 229
Db 911 CACTACTGGCTCTGGACACCGAGCGGATGGCTGGCATAGCTGGCCCATGTCTCATCAG 970
Qy 230 TrpProGlnGlyProSerAlaValAspAlaPheSerTrpGluGluLeuIleValLeu 249
Db 971 TGGCCCAAGGCTCTTTCAGCAGTGTATCTGCTCTTCTCGGAGGAGAAATCTATCTG 1030
Qy 250 ValGlnGlyThrGlnValTyrValPheLeuThrIleGlyGlyTyrThrLeuValSerGly 269
Db 1031 GTCAGGGCACCCAGGTATATGCTTCTCTGACAAAGGAGGAGCTATACCTAGTAGCGGT 1090
Qy 270 TyrProLysArgLeuGluIleValGlyThrProHisGlyIleLeuAspSerVal 289
Db 1091 TATCCGAGCGGCTGGAGAGGAGTGGGACCCCTCATGGATATCTCTGGACTCTGTG 1150
Qy 290 AspAlaAlaPheIleCysProGlySerSerArgLeuHisIleMetAlaGlyArgGlu 309
Db 1151 GATGGGCTTATCTGCTGCTTCTGGCTTCTGCTGCTATATGCTGAGGAGCGCGGCTG 1210
Qy 310 TrpTrpLeuAspLeuIleValSerGlyValAlaGlnAlaThrTrpThrGluLeuProTrpProHis 329
Db 1211 TGGTGGCTGGACCTGAAGTCAAGAGCCCAAGCCAGCTGGACAGAGCTTCTTGGCCCAT 1270
Qy 330 GluIleValAspGlyAlaLeuCysMetGluIleSerLeuGlyProAsnSerCysSerAla 349
Db 1271 GAGAGGTAGACGGAGCGCTTGTGTATGGAAGAGTCCCTTGGCCCTTAATCTATGTTCGCC 1330
Qy 350 AsnGlyProGlyLeuIleIleHisGlyProAsnLeuIleCysTyrSerAspValGlu 369
Db 1331 AATGTCCCGGCTGTGACTCTATCCATGGTCCCATTTGTACTGCTACAGTGTAGTGAG 1390
Qy 370 LysLeuAsnAlaAlaLysAlaLeuProGlnProGlnAsnValThrSerLeuLeuGlyCys 389

Db 1391 ABACTGAATGCAGCCAGGCCCTTCGGCAACCCAGATGTGACCACTCTCTCTGGGCTGC 1450
Qy 390 ThrHis 391
Db 1451 ACTCAC 1456
RESULT 4
US-10-175-523-84
; Sequence 84, Application US/10175523
; Publication No. US20030096264A1
; GENERAL INFORMATION:
; APPLICANT: Brockman, Jeffrey
; APPLICANT: Evans, David
; APPLICANT: Hook, Derek
; APPLICANT: Klimczak, Leszek
; APPLICANT: Laeng, Pascal
; APPLICANT: Palfreyman, Michael
; APPLICANT: Rajan, Prithi
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
; FILE REFERENCE: 3235/10795-US3
; CURRENT APPLICATION NUMBER: US/10/175,523
; CURRENT FILING DATE: 2002-06-18
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/299,151
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 1516
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-175-523-84
Alignment Scores:
Pred. No.: 1,29e-161 Length: 1516
Score: 1556.50 Matches: 296
Percent Similarity: 71.34% Conservative: 35
Best Local Similarity: 63.79% Mismatches: 54
Query Match: 71.24% Indels: 79
DB: 15 Gaps: 6
US-09-900-448-2 (1-391) x US-10-175-523-84 (1-1516)
Qy 1 MetAlaArgValLeuGlyAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
Db 55 ATGGCTAGGACAGTAGTAGTAAATATCTCTGTTATCTGGGCTGTGCTGGTCTGCTGCTG 114
Qy 21 AlaIleAlaThrProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGlu--- 39
Db 115 GCTGTGCTCAACCTCTCTCT-----GCTGCCCATGAGACTGTCTGTAAGGTGAAAT 168
Qy 40 ---ThrIleProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAla 58
Db 169 GGGACCAAGCCAGACTCAGATGTAATCGAACACTGCTCAGATGCTGGAGCTTGGAGCT 228
Qy 59 ThrThrLeuAspAspGlyThrMetLeuPhePheIleGlyGluPheValTrpLysSer 78
Db 229 ACCACCATGATACATATGGACCACTGCTGTTCTTTAAAGGGAGTTTGTGTGGAGGGT 288
Qy 79 HisLysTrpAspArgGluLeuIleSerGluArgTrpIleAsnPheProSerProValAsp 98
Db 289 CACTCAGGATCCGGAGTAAATCTCAGAGAGGTGGAAGAATCCCGTCACCTCAGTGGAT 348
Qy 99 AlaAlaPheArgGlnGlyHisAsnSerValPheIleLeuIleGlyAspLysValTrpVal 118


```
Db 526 GTCTCTTTCTTCCAAAGTAACCGCAAGTGGTTCTGGGACTTTGCCACAAGAACCCCAAG 585
Qy 165 -----
Db 586 GAAAGTTCTGGGCTGCTGTGGGAATTGCATCGCGGCTTGAGTGCGTTGAACGCTAC 645
Qy 165 -----
Db 646 TACTGCTTCAGGGTAACAAGTTCTCTGAGATTAAACCCGTCACAGGAGGTGCTCC 705
Qy 166 -----
Db 706 AGATACCTCTGGATGCCGCTGACTACTTCATATCTGCTGACCATCGAGGTGCCATGCTTC 765
Qy 168 ---ArgAsnGlyThrGlyHisGlyAsnSerThrHisGlyProGluThrMetArgCys 186
Db 766 CTAAGAATGAAGTCTCTGATGGGAATGACCCAT-----CCTATGCTATCGCGCTTGT 819
Qy 187 SerProHisLeuValLeuSerAlaLeuThrSerAspAsnHisGlyAlaThrValAlaPhe 206
Db 820 AACGACGATCTGGCCTGTCTGCACTGCTCTGACCATCGAGGTGCCATGCTTC 879
Qy 207 SerGlyThrHisThrProArgLeuAspThrSerArgAspGlyThrHisSerTrpProLeu 226
Db 880 AGTGGCTCCCACTACTGCTGCTGCACTCGGATCGGCGGTGATGGGCGCATGCTGGCCCAT 939
Qy 227 AlaHisGlnTrpProGlnGlyProSerAlaValAspAlaPheSerTrpGluGluLys 246
Db 940 GCTCATCACTGGCCCAAGCTCTTCAGCAGTAGATGCTGCTTTCTCGGATGAGAA 999
Qy 247 LeuTyroLeuValGlnGlyThrGlnValTyroValPheLeuThrValGlyGlyThrLeu 266
Db 1000 GTCTATCTGATCAGGCGACTCAAGTATATGCTTCTGACGAAAGGGGGGCAATAACCTA 1059
Qy 267 ValSerGlyTyroProLysArgLeuGluLysGluValGlyThrProHisGlyIleLeuLeu 286
Db 1060 GTAAGTGGTTATCCAAAGCGCTGGAGAGCAACTTGGGAGCCTCCCGGATCAGCCTT 1119
Qy 287 AspSerValAspAlaPheLeuCysProGlySerSerArgLeuHisIleMetAlaGly 306
Db 1120 GATACCATAGATGAGCTTTCTCGGCCCTGGTCTTCCAAAGCTCTACGTCACATCAGAA 1179
Qy 307 ArgArgLeuTrpTrpLeuAspLeuLysSerGlyValGlnAlaThrTrpThrGluLeuPro 326
Db 1180 CGGCGGCTTTGGTGGCTGAGCTGAAAGTCAGGAGCCAGCGACATGGCAGAGCTTTC 1239
Qy 327 TrpProHisGlyLysValAspGlyAlaLeuCysMetGluLysSerLeuGlyProAsnSer 346
Db 1240 TGGCCCCATGAGAAAGTGTATGGTGGCTGTGTGGAAAGTCCCTTGGTCCCTACTCA 1299
Qy 347 CysSerAlaAsnGlyProGlyLeuTrpLeuIleHisGlyProAsnLeuTrpCysTrpSer 366
Db 1300 TGCTCTTCCAATGGTCCCACTTGTCTTTATCCATGGGCCCAATTTATCTGCTATAGC 1359
Qy 367 AspValGluLysLeuAsnAlaLysAlaLeuProGlnProGlnAsnValThrSerLeu 386
Db 1360 AGTATAGCAAACTGAATGACGCAAGTCTGCTCAGCCCCAGAAAGTGAACGACATC 1419
Qy 387 LeuGlyCysThr 390
Db 1420 CTTGGCTGCACT 1431
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RESULT 6

US-10-162-335-87

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; Sequence 87, Application US/10162335
; Publication No. US20040009480A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Casmap, Stacie J.
; APPLICANT: Edinger, Shlomit R.
```

```
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Hjalte, Ford
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zehrusen, Bryan D.
; TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Methods
; FILE REFERENCE: 21402-377 B
; CURRENT APPLICATION NUMBER: US/10/162,335
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295,661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/298,285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298,556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299,949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883
; PRIOR FILING DATE: 2001-06-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 201
; SEQ ID NO 87
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)..(775)
US-10-162-335-87

Alignment Scores:
Fred. No.: 7.92e-138 Length: 861
Score: 1338.00 Matches: 255
Percent Similarity: 65.22% Conservative: 0
Best Local Similarity: 65.22% Mismatches: 0
Query Match: 61.24% Indels: 136
DB: 16 Gaps: 1

US-09-900-448-2 (1-391) x US-10-162-335-87 (1-861)

Qy 1 MetAlaArgValLeuGlyAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
Db 10 ATGGCTAGGTTACTGGGAGCACCGCTTGCATGGGGTTGTGGAGCCCTATGCTGGTCTCG 69
Qy 21 AlaIleAlaThrProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThr 40
Db 70 GCCATGGCCACCCCTCTTCTCCGACTAGTGCCTCCATGGGAATGTTCTCTGAGGCGAGACC 129
```

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QY 41 LysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThr 60
DB 130 AAGCCAGACCCAGACGTCAGTGAAGCTGCTCAGATGGCTGGAGCTTTCATGCTACCACC 189
QY 61 LeuAspAsnGlyThrMetLeuPhePheLeuGlyGluPheValTrpLysSerHisLys 80
DB 190 CTGATGACAAATGGAACCATGCTGTTTAA-- 222
QY 81 TrpAspArgGluLeuLeuSerGluArgTrpLysAsnPheProSerProValAspAlaAla 100
DB 222 ----- 222
QY 101 PheArgGlnGlyHisAsnSerValPheLeuLeuLysGlyAspLysValTrpValTrpPro 120
DB 222 ----- 222
QY 121 ProGluLysLysGluLysGlyTyrProLysLeuLeuGlnAspGluPheProGlyIlePro 140
DB 222 ----- 222
QY 141 SerProLeuAspAlaAlaValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeu 160
DB 222 ----- 222
QY 161 PhePheGlnGlyHisGlyHisArgAsnGlyThrGlyHisGlyAsnSerThrHisGly 180
DB 222 ----- 222
QY 181 ProGluTyrMetArgCysSerProHisLeuValLeuSerAlaLeuThrSerAspAsnHis 200
DB 222 ----- 222
QY 201 GlyAlaThrTyrAlaPheSerGlyThrHisTyrTrpArgLeuAspThrSerArgAspGly 220
DB 223 -----GGGACCCACTACTGGCTCTGGACACACCGCGGATGCG 261
QY 221 TrpHisSerTrpProLeuAlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAla 240
DB 262 TGGCATAGCTGGCCCATCTGCTATCAGTGGCCCGGAGGTCCTTCAGCAGTGCATCTGCC 321
QY 241 PheSerTrpGluGluLysLeuValGlnGlyThrGlnValTyrValPheLeuThr 260
DB 322 TTTTCTGGAGAGAAACTCTATCTGGTCCAGGCGACCCAGGTATATGCTTCTCTGACA 381
QY 261 LysGlyGlyTyrThrLeuValSerGlyTyrProLysArgLeuGluLysGluValGlyThr 280
DB 382 AAGGGAGGCTATACCTAGTAAGCGGTTATCCGAGCGGCTGGAGAGGAAAGTCGGAGCC 441
QY 281 ProHisGlyIleLeuLeuAspSerValAspAlaAlaPheIleCysProGlySerSerArg 300
DB 442 CTTCTAGGGAGTTATCTGGACTCTGGAGTGGCGCTTATCTGCCCTGGGTCTTCTCGG 501
QY 301 LeuHisIleMetAlaGlyArgArgLeuTrpTrpLeuAspLeuLysSerGlyValAlaGlnAla 320
DB 502 CTCCATATCATGGCAGGACGGCGGCTGTGGTGGCTGGACCTGAGTCAAGGAGCCCAAGCC 561
QY 321 ThrTrpThrGluLeuProTrpProHisGluLysValAspGlyAlaLeuCysMetGluLys 340
DB 562 ACTGTGACAGACTCTCTTGGCCCATGATGAGAGGAGGAGAGCGCTTGTGTATGAAAG 621
QY 341 SerLeuGlyProAsnSerCysSerAlaAsnGlyProGlyLeuTyrLeuIleHisGlyPro 360
DB 622 TCCCTTGGCCCTAACTCATGTTCCGCCAATGGTGGCTGGTGTACCTCATCCATGGTCCC 681
QY 361 AsnLeuTyrCysTrpSerAspValGluLysLeuAsnAlaAlaLysAlaLeuProGlnPro 380
DB 682 AATTGTACTGCTACAGTATGTGAGAAACTGAAATGAGCAAGGAGGCTTTCGCAACCC 741
QY 381 GlnAsnValThrSerLeuLeuGlyCysThrHis 391
DB 742 CAGAAATGACCACTCTCTGGGCTGCATCTAC 774

```

RESULT 7

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US-09-900-448-3
; Sequence 3, Application US/09900448
; Publication NO. US20030220488A1
; GENERAL INFORMATION:
; APPLICANT: CECARDI, Toni et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001272
; CURRENT APPLICATION NUMBER: US/09/900,448
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: Human
US-09-900-448-3

```

Alignment Scores:

```

Pred. NO.: 2,74e-90 Length: 13737
Score: 921.00 Matches: 195
Percent Similarity: 53.91% Conservative: 5
Best Local Similarity: 52.56% Mismatches: 27
Query Match: 42.15% Indels: 146
DB: 11 Caps: 6

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US-09-900-448-2 (1-391) x US-09-900-448-3 (1-13737)

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QY 165 HisGlyHisArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGlyPro----- 181
DB 10628 CATGGACACCTGAATCCTTAGGAGTGGCCGCAACCCCATGATGTTGGCCTTACCTCG 10687
QY 182 GluTyrMetArgCysSerProHisLeuValLeuSerAlaLeuThrSerAsp----- 198
DB 10688 AACTTAGCCACTGTTTCCACACTTCCCTTTCTTCAGGACCTGCTGATTCACAGTTTC 10747
QY 199 AsnHisGlyAlaThr-----TyrAlaPheSer----- 207
DB 10748 AGCCAGGCACAGTGGCCCAACATGCTGACCAAGTCTTCTCTATTTCTTCCTTCACCT 10807
QY 207 ----- 207
DB 10808 GGCTCTTCCATCTTGGCTCTGGATGCATTTCTCTCTCTCATGACTCATTTTCTGCATT 10867
QY 207 ----- 207
DB 10868 CATCACTAGCCTCTTCTCTGCTGGCTTCTGCCAGCGGCCCTAGACCAACCTATGATAT 10927
QY 208 -----GlyThrHisTyrTrpArgLeuAspThrSerArgAspGlyTrpHisSerTrpPro 225
DB 10928 TCCACAGGAGACCCACTACTGCGCTCTGGACACACCGCGGATGGCTGGCATAGCTGGGCC 10987
QY 226 IleAlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAlaPheSerTrpGluGlu 245
DB 10988 ATGTCTCATCAGTGGCCCGCCAGGTCTTCCAGCAGTGGATGCTGCTCTTCTTCTGGGAAGA 11047
QY 246 LysLeuTyrLeuVal----- 250
DB 11048 AAACCTCTATCTGGT-CCAGGTCTGTATTGGGGGAGAGGCTTGGAGTAGAGACTGGGACAA 11106
QY 251 -----GlnGlyThrGlnValTyrVal 257
DB 11107 GCATATCCCACTCTGTATTATTACCATCTTTTGTCTCCAGGACCCAGGATATATGTC 11166
QY 258 PheLeuThrLysGlyGlyTyrThrLeuValSerGlyTyrProLysArgLeuGluLysGlu 277
DB 11167 TTCTCTGACAAAGGAGGCTTATACCTCTAGTAGCGGTATTCGGAAGCGGCTGGAGAAGAA 11226
QY 278 ValGlyThrProHisGlyIleLeuAspSerValAspAlaAlaPheIleCysProGly 297
DB 11227 GTGCGGACCCCTCATGGGATATATCTGTGACTCTGTGGATGGCGCTTTTATCTGCCCTGGG 11286

```


Qy 101 PheArgGlnGlyHisAsnSerValPheLeuIleLysGlyAspLysValTrpValTrpPro 120
Db 314 TTCGTCAGGTCACACAGTGTCTTTCTGATCAAGGGGACAAAGTCTGGGTATACCT 373
Qy 121 ProGluLysGlyLysGlyLysGlyTrpProLysLeuLeuGlnAspGluPhe 136
Db 374 CCTGAAGAAGAGGAGGAAGGATACCCAAAGTTGCTCCAGATGAATTT 421

RESULT 10
US-09-918-995-31395
; Sequence 31395, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31395
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(492)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31395

Alignment Scores:
Pred. No.: 2,61e-69 Length: 492
Score: 714.00 Matches: 135
Percent Similarity: 93.84% Conservative: 2
Best Local Similarity: 92.47% Mismatches: 9
Query Match: 22.68% Indels: 1
Gaps: 0

US-09-900-448-2 (1-391) x US-09-918-995-31395 (1-492)

Qy 1 MetAlaArgValLeuGlyAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
Db 56 ATGGTAGGGTACTGGAGACCCGATGCATGCTGGGTTGTGGAGCCTATGCTGGTCTCTG 115
Qy 21 AlaIleAlaThrProLeuProThrSerAlaHisGlyAsnValAlaGluGlyGluThr 40
Db 116 GCCATTGCCACCCCTCTTCTCCGACTAGTGCCTATGGGAATGTTGCTGAAGGGAGACC 175
Qy 41 LysProAspProAspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThr 60
Db 176 AAGCAGACCCGACGTCGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 235
Qy 61 LeuAspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHisLys 80
Db 236 CTGGATGACAAATGGAAACCATGCTGTTTAAAGGGGAGTGTGTGGAGAGTGCACAA 295
Qy 81 TrpAspArgGluLeuLysSerGluArgTrpLysAsnPheProSerProValAspAla 100
Db 296 TGGGACCGGGAGTTAATCTTCACAGATGGAGAAATTTCCCGAGCCCTGTGGATGCTGCA 355
Qy 101 PheArgGlnGlyHisAsnSerValPheLeuLysGlyAspLysValTrpValTrpPro 120
Db 356 TTCGTCAGGTCACACAGTGTCTTCTGATCAAGGGGACACAGTCTGATATACCT 415
Qy 121 ProGluLysGlyLysGlyTrpProLysLeuGlnAspGluPheProGlyLeuPro 140
Db 416 CCTGANNAGAGGAGACAGATACCCAAAGTGTCTCCAAAGTGAATTCAGTGATC-CCA 474
Qy 141 SerProLeuAspAla 146

Db 475 TACCCACTGGATCCAGCN 492

RESULT 11
US-09-918-995-30754
; Sequence 30754, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30754
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(488)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-30754

Alignment Scores:
Pred. No.: 9,19e-69 Length: 488
Score: 709.00 Matches: 130
Percent Similarity: 80.00% Conservative: 6
Best Local Similarity: 76.47% Mismatches: 8
Query Match: 32.45% Indels: 26
Gaps: 2

US-09-900-448-2 (1-391) x US-09-918-995-30754 (1-488)

Qy 120 ProProGluLysLysGlyLysGlyTrpProLysLeuLeuGlnAspGluPheProGlyLe 139
Db 57 CCTCCAGG-----TACCCGGGATGTCGAGACTACTTTCATGCCCTGC 101
Qy 140 ProSerProLeuAspAlaAlaValGluCysHisArgGlyGluCysGlnAlaGluGlyVal 159
Db 102 CTGCG-----AGAGCCCATGGACACAGCAATGGGACTGGCCATGGGAACAGTACCCACCAT 158
Qy 160 LeuPhePheGlnGlyHisGlyHisArgAsnGlyThrGlyHisGlyAsnSerThrHisHis 179
Db 108 -----AGAGCCCATGGACACAGCAATGGGACTGGCCATGGGAACAGTACCCACCAT 158
Qy 180 GlyProGluTrpMetArgCysSerProHisLeuValLeuSerAlaLeuThrSerAspAsn 199
Db 159 GGCCTCAGTATATGCGCTGTAGCCCATCTAGTCTGTCTGTGCTGCTGCTGCTGCTGCTGCT 218
Qy 200 HisGlyAlaThrTrpAlaPheSerGlyThrHisTrpArgLeuAspThrSerArgAsp 219
Db 219 CATGGTGCACCTATGCTTCAGTGGGCCACCTACTTGGGATGGACACCCAGCGCGGAT 278
Qy 220 GlyTrpHisSerTrpProIleAlaHisGlnTrpProGlnGlyProSerAlaValAspAla 239
Db 279 GGCTTGGCATAGCTGGCCCATTTGCTCATAGTGGGCCCTCCCTTCCAGCAGTGGATGCT 338
Qy 240 AlaPheSerTrpGluGluLysLeuTrpValGlnGlyThrGlnValTrpValPheLeu 259
Db 339 GCCTTTTCTCGGAAGAAATACTCTATCTGTCGAGGCCACCCAGGTATATGCTCTCTG 398
Qy 260 ThrLysGlyGlyTrpThrLeuValSerGlyTrpProLysArgLeuGluLysGluValGly 279
Db 399 ACAAGGAGGAGCTATACCTAGTAAGCGTTATCCGAAGCGGCTGGAGAGGAGACGCGG 458
Qy 280 ThrProHisGlyLysLeuAspSerVal 289
Db 459 ACCCTCATGGATTTATGCTGGACTCTCTG 488

RESULT 13

US-09-918-995-7738

Alignment Scores:
Pred. No.: 1.24e-51 Length: 384
Score: 552.50 Matches: 106
Percent Similarity: 86.18% Conservative: 0
Best Local Similarity: 86.18% Mismatches: 1
Query Match: 25.29% Indels: 17
DB: 10 Gaps: 1

US-09-900-448-2 (1-391) x US-09-918-995-7738 (1-384)

Qy 1 MetAlaArgValLeuGlyValAlaProValAlaLeuGlyLeuTrpSerLeuCysTrpSerLeu 20
Db 17 ATGGTGTAGGTACTGGGACACCCCTTGCACCTGGGGTGTGGAGCCTATGCTGTCTCTG 76
Qy 21 AlaileAlaThrProLeuProThr----- 29
Db 77 GCCATTGCCACCCCTCTCTCCCTG-AGTAAAGCTGGGACTAGAGCGAAGGATTGAGT 135
Qy 30 -----SerAlaHisGlyAsnValAlaGluGlyGluThrLysProAspPro 44
Db 136 TCTGGCTAGGAGTACTGCTCCCATGGGATGTTGCTGAAGCGAGACCCAGCCAGCCCA 195
Qy 45 AspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThrLeuAspAspAsn 64
Db 196 GAGCTGACTGAACCGTCTCAGATGGCTGGAGCTTTGATGCTTACCACCCCTGGATGACAAT 255
Qy 65 GlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHisLysTrpAspArgGlu 84
Db 256 GGAACCATGCTCTTTTAAAGGGGAGTTTGTGGAGAGTCAAAATGGGACCGGGAG 315
Qy 85 LeuileSerGluArgTrpLysAsnPheProSerProValAspAlaAlaPheArgGlnGly 104
Db 316 TTAATCTCAGAGAGTGGAGAGATTTCCCAAGCCCTGTGGATGCTGCAATTCGTCAGGT 375
Qy 105 HisAsnSer 107
Db 376 CACAACAGT 384

RESULT 15

US-09-918-995-32181
; Sequence 32181, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: FROM VARIOUS CDNA LIBRARIES
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32181
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(473)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32181

Alignment Scores:
Pred. No.: 2.64e-50 Length: 473
Score: 541.50 Matches: 99
Percent Similarity: 73.83% Conservative: 11
Best Local Similarity: 66.44% Mismatches: 16
Query Match: 24.78% Indels: 23
DB: 10 Gaps: 2

US-09-900-448-2 (1-391) x US-09-918-995-32181 (1-473)

Qy 109 PheLeuileLysGlyAspLysValTrpValTrpProProGluLysLysGlu-----Lys 126
Db 89 TACTGCTTCAGGGTAACCAATTCCTCGCTTCGACCCCTGTACGGGGAGAGTGCCTCCC 148
Qy 127 GlyTrpProLysLeuLeuGlnAspGluPheProGlyLeuProSerProLeuAspAlaAla 146
Db 149 AGGTACCGCGGGATGTCGAGAGACTTCTATGCCCCCTGGC----- 193
Qy 147 ValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPheGlnGlyHisGly 166
Db 194 -----AGAGGCCATGGA 205
Qy 167 HisArgAsnGlyThrGlyHisGlyAsnSerThrHisGlyProGluTrpMetArgCys 186
Db 206 CACAGGAATGGGACTGGCCATGGGACAGTACCACCATGGCCCTGATATATGCGCTGT 265
Qy 187 SerProHisLeuValLeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTrpAlaPhe 206
Db 266 AACCCACATCTAGTCTTGTCTGCACTGACGTCTGACACCATGGTGCACCTATGCTTC 325
Qy 207 SerGlyThrHisTrpTrpArgLeuAspThrSerArgAspGlyTrpHisSerTrpProle 226
Db 326 AGTGGGACCCACTACTGCGCTGGACACACCGCGGATGCTGGCATAGCTGGCCCAT 385
Qy 227 AlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAlaPheSerTrpGluGluLys 246
Db 386 GCTCATCATGTCGCCCCAGGGTCTTTCACGACGTGATGCTGCTTTCTCTGGAGAGAAAA 445
Qy 247 LeuTrpLeuValGlnGlyThrGlnVal 255
Db 446 CTCTATCTGTTCCAGGGCACCCAGGTA 472

Search completed: June 8, 2004, 07:23:56
Job time : 545 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2004, 02:37:18 ; Search time 95 Seconds
(without alignments)
2284.061 Million cell updates/sec

Title: US-09-900-448-2
Perfect score: 2185
Sequence: 1 MAEVLGAPVALGWSLWNSL.....NAAKALPQPONVTSLLGCTH 391

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 6

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -QMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFM=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0900448.cg2n_1_56 @runat_07062004_094658_20469 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

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3: /cg2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cg2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cg2_6/ptodata/2/ina/PTCUS.COMB.seq.*
6: /cg2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	202.5	9.3	1410	3	US-08-068-392-1
2	202.5	9.3	1410	3	US-08-396-988-1
3	200.5	9.2	3530	3	US-08-704-711A-10
4	200.5	9.2	3530	4	US-09-521-220-10
5	187.5	8.6	2260	1	US-07-794-393-3
6	187.5	8.6	2260	1	US-08-008-711-3
7	187.5	8.6	1717	1	US-08-229-515A-12
8	185	8.6	1717	1	US-08-645-865-12
9	185	8.5	3807	2	US-08-816-755-1
10	185	8.5	3807	3	US-09-090-673-1
11	183.5	8.4	2223	4	US-09-178-002-3
12	183.5	8.4	2223	4	US-09-023-655-1040

13	183.5	8.4	2247	4	US-09-023-655-1410
14	183.5	8.4	2256	1	US-07-794-393-1
15	183.5	8.4	2256	1	US-08-001-711-1
16	183.5	8.4	2314	1	US-09-178-002-1
17	181.5	8.3	1970	4	US-09-023-655-1264
18	181.5	8.3	1981	4	US-09-484-970B-62
19	177	8.1	1160	1	US-07-780-973-15
20	177	8.1	1434	4	US-09-023-655-1174
21	177	8.1	1801	4	US-09-023-655-1374
22	176	8.1	1521	4	US-08-994-689C-18
23	176	8.1	2792	4	US-08-994-689C-8
24	174	8.0	1923	3	US-09-294-841-1
25	167.5	7.7	1233	4	US-09-171-545-9
26	167.5	7.7	1238	4	US-09-171-545-10
27	167.5	7.7	1524	4	US-09-171-545-7
28	167.5	7.7	2264	4	US-09-171-545-22
29	160.5	7.3	3403	3	US-08-448-489-2
30	157.5	7.2	2049	4	US-09-171-545-23
31	156	7.1	2275	4	US-09-391-104-1
32	155.5	7.1	3437	3	US-08-704-711A-9
33	155.5	7.1	3437	4	US-09-521-220-9
34	155.5	7.1	3456	3	US-08-704-711A-8
35	155.5	7.1	3456	4	US-09-521-220-8
36	154	7.0	1257	4	US-09-171-545-11
37	154	7.0	1272	4	US-09-171-545-12
38	154	7.0	1551	4	US-09-171-545-8
39	154	7.0	3813	4	US-07-757-022B-43
40	154	7.0	3936	4	US-07-757-022B-41
41	154	7.0	3942	4	US-07-757-022B-141
42	154	7.0	3945	4	US-07-757-022B-49
43	154	7.0	3963	4	US-07-757-022B-45
44	154	7.0	3963	4	US-07-757-022B-59
45	154	7.0	4065	4	US-07-757-022B-47

ALIGNMENTS

RESULT 1

US-08-068-392-1
; Sequence 1, Application US/08068392
; Patent No. 6150152
; GENERAL INFORMATION:
; APPLICANT: Shapiro, Steven M.
; TITLE OF INVENTION: Human Macrophage Metalloproteinase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,392
; FILING DATE: 19930528
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J. 25275
; REGISTRATION NUMBER: 07-24(12406)A
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1410 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double

GENERAL INFORMATION:
APPLICANT: Shapero, Steven M.
TITLE OF INVENTION: Human Macrophage Metalloproteinase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,988
FILING DATE: 01-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,392
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25275
REFERENCE/DOCKET NUMBER: 07-24 (12406)A
TELEPHONE: (314)694-3117
TELEFAX: (314)694-5435
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1410
US-08-396-988-1

Alignment Scores:
Pred. No.: 1,72e-10 Length: 1410
Score: 202.50 Matches: 66
Percent Similarity: 36.78% Conservative: 23
Best Local Similarity: 27.27% Mismatches: 90
Query Match: 9.27% Indels: 63
DB: Gaps: 10

US-09-900-448-2 (1-391) x US-08-068-392-1 (1-1410)
QY 30 SerAlaHisGlyAsnValAlaGluGlyThrLysProAspProAspValThrGlu--- 48
DB 778 TCCTGTATGGAGACCCAAAGAGAACCAACGCTTGCCAAATCTCGACAAATTCAGAACCA 837

QY 49 ---ArgCysSerAspGlyTrpSerPheAspAlaThrLeuAspAspAsnGlyThrMet 67
DB 838 GCTCTCTGTGACCCCAATTTGAGTTTGTGCTGCTACCTACCGTGGGAAT---AAGATC 894

QY 68 LeuPhePheLysGlyGluPheValTrp-----LysSerHisLysTrpAspArg 83
DB 895 TTTTCTTCAAGACAGAGGTTCTTCTGGCTGAAGGTTCTGAGAGACCAAGACCAAGTGT 954

QY 84 GluLeuIleSerGluArgTrpLysAsnPheProValAspAlaAlaPheArg--- 102
DB 955 AATTTAAATTTCTTCTTATGGCCAACTTGGCATCTGGCATCTGAGCTGCTATGAAAT 1014

QY 103 GlnGlyHisAsnSerValPheLeuIleLysGlyAspLysValTrpValTrpProGlu 122
DB 1015 GAAGCCAGAAATCAAGTTTCTTTTAAAGATGACAAATACTGGTTAATTAGCAATTTA 1074

QY 123 LysLysGluLysGlyTyPrProLysLeuLeuGlnAsp---GluPheProGlyIleProSer 141
US-09-900-448-2 (1-391) x US-08-396-988-1 (1-1410)

Alignment Scores:
Pred. No.: 1,72e-10 Length: 1410
Score: 202.50 Matches: 66
Percent Similarity: 36.78% Conservative: 23
Best Local Similarity: 27.27% Mismatches: 90
Query Match: 9.27% Indels: 63
DB: Gaps: 10

TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1410
US-08-068-392-1

Alignment Scores:
Pred. No.: 1,72e-10 Length: 1410
Score: 202.50 Matches: 66
Percent Similarity: 36.78% Conservative: 23
Best Local Similarity: 27.27% Mismatches: 90
Query Match: 9.27% Indels: 63
DB: Gaps: 10

US-09-900-448-2 (1-391) x US-08-068-392-1 (1-1410)
QY 30 SerAlaHisGlyAsnValAlaGluGlyThrLysProAspProAspValThrGlu--- 48
DB 778 TCCTGTATGGAGACCCAAAGAGAACCAACGCTTGCCAAATCTCGACAAATTCAGAACCA 837

QY 49 ---ArgCysSerAspGlyTrpSerPheAspAlaThrLeuAspAspAsnGlyThrMet 67
DB 838 GCTCTCTGTGACCCCAATTTGAGTTTGTGCTGCTACCTACCGTGGGAAT---AAGATC 894

QY 68 LeuPhePheLysGlyGluPheValTrp-----LysSerHisLysTrpAspArg 83
DB 895 TTTTCTTCAAGACAGGTTCTTCTGGCTGAAGGTTCTGAGAGACCAAGACCAAGTGT 954

QY 84 GluLeuIleSerGluArgTrpLysAsnPheProValAspAlaAlaPheArg--- 102
DB 955 AATTTAAATTTCTTCTTATGGCCAACTTGGCATCTGGCATCTGAGCTGCTATGAAAT 1014

QY 103 GlnGlyHisAsnSerValPheLeuIleLysGlyAspLysValTrpValTrpProGlu 122
DB 1015 GAAGCCAGAAATCAAGTTTCTTTTAAAGATGACAAATACTGGTTAATTAGCAATTTA 1074

QY 123 LysLysGluLysGlyTyPrProLysLeuLeuGlnAsp---GluPheProGlyIleProSer 141
DB 1075 AGACGAGACCAATATCCCAAGACATACATCTTTGGTTTCTTAACTTGTGAAA 1134

QY 142 ProLeuAspAlaAlaValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPhe 161
DB 1135 AAAATTTGATGACGCTGTT-----LysSerHisLysTrpAspArg 1152

QY 162 PheGlnGlyHisGlyHisArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGlyPro 181
DB 1153 -----TTTAAACCCA 1161

QY 182 GluTyTrpMetArgCysSerProHisLeuValLeuSerAlaLeuThrSerAspAsnHisGly 201
DB 1162 CGTTTTTATAGG-----LysSerHisLysTrpAspArg 1173

QY 202 AlaThrTyTrpAlaPheSerGlyThrHisTyTrpArgLeuAspThrSerArgAsp----- 219
DB 1174 ---ACCTACTTCTTTGTAGATAACCAAGTATGGAGTATGATGAAGGACAGATGATG 1230

QY 220 -----GlyTrpHisSerTrpProIleAlaHisGlnTrpProGlnGlyProSerAlaVal 237
DB 1231 GACCTGGTTATCCCAACTGATACCAAGACTTCCAGGAATCGGCCCTAAA---ATT 1287

QY 238 AspAlaAlaPheSerTrpGluGluLys---LeuTyTrpLeuValGlnGlyThrGlnValTy 256
DB 1288 GATGCAGTCTTCTTCTTAAACCAAAATACTACTATTCTTCTCAAGGATCTAAACCAATTT 1347

QY 257 ValPhe 258
DB 1348 GAATAT 1353

RESULT 2
US-08-396-988-1
; Sequence 1, Application US/08396988
; Patent No. 6204043

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DB 1075 AGACGAGACCAAAATATCCAGAGCATACATCTTTTGGTTTCTTAACCTTGTGAAA 1134
QY 142 ProLeuAspAlaValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPhe 161
DB 1135 AAAATGATGCAGCTTT 1152
QY 162 PheGlnGlyHisGlyHisArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGlyPro 181
DB 1153 -----TTTAAACCA 1161
QY 182 GluTyrMetArgCysSerProHisLeuValLeuSerAlaLeuThrSerAspAsnHisGly 201
DB 1162 CGTTTATAGG 1173
QY 202 AlaThrTyrAlaPheSerGlyThrHisTyrTrpArgLeuAspThrSerArgasp 219
DB 1174 ---ACCTACTCTTTCTAGATAACCACTGATGGAGTATGATGAAGGAGACAGATGATG 1230
QY 220 -----GlyTyrHisSerTrpProIleAlaHisGlnTrpProGlnGlyProSerAlaVal 237
DB 1231 GACCCCTGGTTATCCAACTGATTACCAAGAACTTCCAAAGGAATCGGCTTAA 1287
QY 238 AspAlaAlaPheSerTrpGluGluLys----LeuTyrLeuValGlnGlyThrGlnValTyr 256
DB 1288 GATGCAGTCTCTTATTCTAAACAAATACTACTATTCTTCCAGGATCTTAAACCAATT 1347
QY 257 ValPhe 258
DB 1348 GAATAT 1353
```

RESULT 3

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US-08-704-711A-10
Sequence 10, Application US/08704711A
Patent No. 6114159
GENERAL INFORMATION:
APPLICANT: WILL, Horst
TITLE OF INVENTION: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
```

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TELEX: 904136
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3530 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-10

Alignment Scores:
Pred. No.: 1,038-09 Length: 3530
Score: 200.50 Matches: 90
Percent Similarity: 33.33% Conservative: 37
Best Local Similarity: 23.62% Mismatches: 141
Query Match: 9.18% Indels: 113
DB: 3 Gaps: 18

US-09-900-448-2 (1-391) x US-08-704-711A-10 (1-3530)
QY 25 ProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThrLysProAspPro 44
DB 1051 CCCCAGCCACCAACCCCA-----GGTGGAAAGCCAGAGCGGCCCCCAAGCGCGGCC 1104
QY 45 AspValThrGluArgCysSer-----AspGly 53
DB 1105 CCAGTCCAGCCCGCCGACACAGAGCGGCCGACCATGATGCGTCTTCAAGGCGCG 1164
QY 54 TrpSerPheAspAlaThrThrLeuAspAspAsnGlyThrMetLeuPhePheLysGlyGlu 73
DB 1165 ---GACTTTGACACAGTGGCCATG---CTTCGCGGGGAGATGTTCTGTGTTCAAGGCGCG 1218
QY 74 PheValTrpLysSerHisLysTrpAspArgGluLeu-----IleSer 87
DB 1219 TGGTTCTGCGAGTC---CGGCACAAACCGCTCTGGACAACTATCCCATGCCCATCGGG 1275
QY 88 GluArgTrpLysAsnPheProSerProValAspAlaAlaPheArgGlnGlyHisAsnSer 107
DB 1276 CACTTCTGGCGTGTCTGCCCGTGCATCATCTGCTACAGAGCGCCAGACGCTGCT 1335
QY 108 ValPheLeuIleLysGlyAspLysValTrpValTyrProGluLysLysGlyLys 127
DB 1336 TTTGTCTTTTCAAAGGTGACCGCTACTGCTCTTCGAGAAGCGAACCTGGAGCGCGCG 1395
QY 128 TyrProLysLeuLeuGlnAspLysPheProGlyIlePro---SerProLeuAspAlaAla 146
DB 1396 TACCCAGAGCGCGCTACAGCATGATGCGCTGGCATCCCTATGACCGCATTCACAGCGCC 1455
QY 147 ValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPhePheGlnGlyHisGly 166
DB 1456 ATC-----TGGTGGAGGCCACAGCG 1476
QY 167 His-----ArgAsnGlyThrGlyHisGly 174
DB 1477 CACACCTTCTTCTCCAAAGAGGACAGGTACTGGCGCTTCAACAGAGGACACAGCGTGA 1536
QY 175 AsnSerThrHisHisGlyPro-----GluTyrMetArgCysSerProHisLeu 190
DB 1537 GACCTGGGTACCCCAAGCCCATCATCTGCTGGAGGGATCCCTGCCCTCCCTAAA--- 1593
QY 191 ValLeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPheSerGlyThrHis 210
DB 1594 -----GGGGCTTCTCTGAGCAATGACGAGCTACCTACTCTACAAAGGCCCAAA 1647
QY 211 TyrTrpArgLeuAspThrSerArg-AspGlyTrpHis----- 222
DB 1648 TACTGAAATTCGACAAATGAGCGCTCGGATGGAGCGCGGTACCCCAAGTCCATCTG 1707
QY 223 -----SerTrpProIleAlaHisGlnTrpProGlnGlyProSerAlaValAspAla 240
DB 1708 CGGCACTTTCATGGCTGCCAGGAGCAGCGTGGAGCGAGGCCCGCATGGCGCCG--- 1759
QY 240 aPheSerTrpGluGluLysLeuTyrLeuValGlnGlyThrGlnValTyrValPheLeuTh 260
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935 ATG---CTGAGGGGAAATTCCTATTCTTTAAAGACAGCACTTCTGGCGTAGAACCCAG 991
 81 TTPAspArgGlu-----LeuIleSerGluArgTTPAspAsnPhenProSerPro 96
 992 TGGATCCGAGCCGATTCATTTGATTTGAGCATTTTGGCCCTCTCTCTTCCTTCAGGC 1051
 97 ValAspAlaAlaPheArgGlnGlyHis---AsnSerValPheLeuIleLysGlyAspLys 115
 1052 ITAGATGTCGCTATGAGCAATAACAGGACAGAGTCTTGATTTTAAAGGAAGTCA 1111
 116 ValTTPVal----- 118
 1112 TCTGGCGAGTCCGAGGAATGAAGTCCAGCAGCTTACCCAAAGAGGATCCACACTCTT 1171
 119 ---TyrProPro-----GluLysLys--- 124
 1172 GCGTTTCTCCGCCACCGCTGAAGAAGATTGATGACGCTGTTTTTGAAGAGGAAGAAG 1231
 125 -----Glu 125
 1232 AGTATTCTTTGTAGTGACAAATACGAGATTGATGACAGACAGCAGCTTATGGAT 1291
 126 LysGlyTyrProLysLeuLeuGlnAspGluPheProGlyIleProSerProLeuAspAla 145
 1292 AAAGGCTTCCGAGACTGATACAGATGACTTCCAGGAGATTGAGCCACAGTGTGATGCT 1351
 146 AlaValGluCysHisArgGlyGlyCysGlnAlaGluGlyValLeuPhePhe 162
 1352 GGTGTA-----CATGCATTGGGGTTTTTTTATTTC 1381

RESULT 9

US-08-816-755-1
 ; Sequence 1, Application US/08816755
 ; Patent No. 5837508
 ; GENERAL INFORMATION:
 ; APPLICANT: Arleth, Anthony
 ; APPLICANT: Arnold, Anne
 ; APPLICANT: Shabon, Usman
 ; TITLE OF INVENTION: No. 5837508el Membrane-Type Matrix
 ; TITLE OF INVENTION: Metalloproteinase-5 Gene
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY:
 ; ZIP: 19406
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/816,755
 ; FILING DATE: 05-MAR-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hag, William T
 ; REGISTRATION NUMBER: 34,344
 ; REFERENCE/DOCKET NUMBER: GH50007
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-270-5219
 ; TELEFAX: 610-270-4026
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3807 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single

TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-08-816-755-1
 Alignment Scores:
 Pred. No.: 3.89e-08 Length: 3807
 Score: 185.00 Matches: 87
 Percent Similarity: 30.41% Conservative: 31
 Best Local Similarity: 22.42% Mismatches: 123
 Query Match: 8.47% Indels: 147
 DB: 2 Gaps: 17
 US-09-900-448-2 (1-391) x US-08-816-755-1 (1-3807)
 QY 25 ProLeuProProThrSerAlaHisGlyAsnValAlaGluGlyGluThrLysProAspPro 44
 DB 532 CTTGGCGCGCCCTCG-----GGGAGCCGCCATCCACCA 567
 QY 45 AspValThrGluArgCysSerAspGlyTTPSerPheAspAlaThrThrLeuAspAspAsn 64
 DB 568 GGCACCAACCCACATCTGTGACGGC-----AACTTC 600
 QY 65 GlyThrMetLeuPhePheLysGlyGlu---PheValTTPLysSerHisLysTTPAspArg 83
 DB 601 AACACAGTGGCCCTCTTCCGGGCGGAGATGTTGTCTTAAGAT---CGCTGGTCTTGG 657
 QY 84 GluLeu-----IleSerGluArgTTPLys 91
 DB 658 CGTTCGCCAATAACCGAGTGCAGAGGGGTACCCCATGCAGATCGACGAGTCTTGAAG 717
 QY 92 AsnPheProSerProValAspAlaAlaPheArgGlnGlyHisAsnSerValPheLeuLeu 111
 DB 718 GGCCTGCTGCGCCGATCGACGAGCCTATGAAAGGGCGGATGGGAGATTGTCTTCTTC 777
 QY 112 LysGlyAspLysValTTPValTTPProGluLysLysGlyLysGlyLysTTPProLysLeu 131
 DB 778 AAAGTGACAGTATGTTGGTGTTTAAGAGAGTGGTGGAGCTGGGTATCCCCACACAGC 837
 QY 132 LeuGlnAspGluPheProGlyIleProSerProLeuAspAlaAlaValGluCysHisArg 151
 DB 838 CTGGGGGAG-----CTG 849
 QY 152 GlyLysCysGlnAlaGluGlyValLeuPhePheGlnGlyHisGlyHisArgAsnGlyThr 171
 DB 850 GGCAGCTCTTTGCC-----CGTAGGC--- 873
 QY 172 GlyHisGlyAsnSerThrHisGlyProGluTyrMetArgCysSerProHisLeuVal 191
 DB 874 -----ATT 876
 QY 192 LeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPheSerGlyThrHisTyr 211
 DB 877 GACACAGCTCTGGCGCTGGGAACCTGTGGGCAAGACCTACTTTTCAAAGGGGAGCGGTAC 936
 QY 212 TTPArgLeuAspThrSerArg-----AspGlyTTPHisSerTTPProIleAlaHis 228
 DB 937 TGGCGCTACAGCGAGGAGCGCGGCGCCACCGCCCTGCTACCTTAAGCCCATCACC--- 993
 QY 229 GlnTTPProGlnGlyProSerAlaValAspAlaPheSerTTPGluGlu-----Lys 246
 DB 994 GTGTGGAAGGGCATCCACAGGCTCCCAAGAGGCTTCATCAGCAGGAAGGATATTAC 1053
 QY 247 LeuTyrLeuValGlnGlyThrGlnValTyrValPheLeuThrLysGlyTyrThrLeu 266
 DB 1054 ACCTATTCTCAAGGGCGGGAGTACTGGAGATTGACAC----- 1095
 QY 267 ValSerGlyTyrProLysArgLeuGluLysGluValGlyThrProHisGlyIleLeuLeu 286
 DB 1096 -----CAGAACTGAGCGTGGAGCGAGCTACCCGCGCAACATCTCGGT 1140
 QY 287 AspSerValAspAlaAlaPheIleCysProGlySerArgLeuHisIleMet-AlaG 306
 DB 1141 GAC-----TGGATGGGCTGC 1155

Qy 306 yArgArgLeuTrpTrpLeuAspLeuLysSerGlyVala-----GlnAlaThrTrpThrGl 324
 Db 1156 AACCAAGAGGAGGTGGAGCGCGGAGCGCGGTGCCCCAGGACGAGCGTGGACATC 1215
 Qy 324 u-----LeuProTrpProHisGluLysValas 333
 Db 1216 ATGGTGACCATCAAGATGTCCGGGTCCGTGAACGCGGTGGCGGTGCTCA----- 1267
 Qy 333 pGlyAlaLeuCysMetGluLysSerLeuGlyProAsnSerCysSerAlaAlaanglyProGl 353
 Db 1268 -----TCCCTGTCATCCTGTCCTCCCTTCGCATCC----- 1294
 Qy 353 yLeuTyrlleuIleHisGlyProAsnLeuTyrcysTyrsSerAspValGluLysLeuAsnAl 373
 Db 1295 -----TGGTGCTGTCTACACCACTTCCAGTTCAG 1326
 Qy 373 aAlaLysAlaLeuProGlnPro 380
 Db 1327 AACCAAGACAGCGCTCAGCCT 1348

RESULT 10

US-09-090-673-1
 ; Sequence 1, Application US/09090673
 ; Patent No. 6214600
 ; GENERAL INFORMATION:
 ; APPLICANT: Arleth, Anthony
 ; APPLICANT: Arnold, Anne
 ; APPLICANT: Shabon, Usman
 ; TITLE OF INVENTION: No. 6214600el Membrane-Type Matrix
 ; TITLE OF INVENTION: Metalloproteinase-5 Gene
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ratner & Prestia
 ; STREET: P.O. Box 980
 ; CITY: Valley Forge
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19482
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/090,673
 ; FILING DATE: 3-June-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Prestia, Paul F.
 ; REGISTRATION NUMBER: 23,031
 ; REFERENCE/DOCKET NUMBER: GH50007-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-407-0700
 ; TELEFAX: 610-407-0701
 ; TELEX: 846169
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3807 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-09-090-673-1

Alignment Scores: 3.88e-08 Length: 3807
 Pred. No.: 185.00 Matches: 87
 Score: 30.41% Conservative: 31
 Percent Similarity: 22.42% Mismatches: 123
 Best Local Similarity:

Query Match: 8.47% Indels: 147
 DB: 3 Gaps: 17
 US-09-900-448-2 (1-391) x US-09-090-673-1 (1-3807)
 Qy 25 ProLeuProThrSerAlaHisGlyAsnValaLalaGluGluThrLysProAspPro 44
 Db 532 CCTCGGCGCGCTCG-----GGGACCGCGCCATCCACACCA 567
 Qy 45 AspValThrGluArgCysSerAspGlyTrpSerPheAspAlaThrThrLeuAspAsn 64
 Db 568 GGCACCAACCAACATCTCTGACGCG-----AACTTC 600
 Qy 65 GlyThrMetLeuPhePheLysGlyGlu---PheValTrpLysSerHisLysTrpAspArg 83
 Db 601 AACACAGTGGCCCTCTTCCGCGGAGATCTTGTCTTTAAGGAT---CGTGGTCTCG 657
 Qy 84 GluLeu-----IleSerGluArgTrpLys 91
 Db 658 CGTCTGCGCAATAACGAGTGCAGAGGGGTACCCCATGCAGATCGAGCGTTCTGGAG 717
 Qy 92 AsnPheProSerProValAspAlaPheArgGlnGlyHisAsnSerValPheLeuIle 111
 Db 718 GGCCTGCTGCCGATCGACGAGCCCTATGAAAGGCGCGATGGAGATTGTCTCTTC 777
 Qy 112 LysGlyAspLysValTrpValTyProGluLysLysGlyLysGlyTyProLysLeu 131
 Db 778 AAAGGTGACAGTATTGGGTGTTAAGGAGGTGCGGTGGGTACCCCCACAGC 837
 Qy 132 LeuGlnAspGluPheProGlyIleProSerProLeuAspAlaAlaValGluCysHisArg 151
 Db 838 CTGGGGGAG-----CTG 849
 Qy 152 GlyGluCysGlnAlaGluGlyWalLeuPhePheGlnGlyHisGlyHisArgAsnGlyThr 171
 Db 850 GGCAGCTGTTGGCC-----CGTGAAGGC--- 873
 Qy 172 GlyHisGlyAsnSerThrHisGlyProGluTyMetArgCysSerProHisLeuVal 191
 Db 874 -----ATT 876
 Qy 192 LeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyAlaPheSerGlyThrHisTy 211
 Db 877 GACACAGCTCTGCGTGGGAACCTGTGGCGAAGACCTACTTTTCAAAGGCGAGCGGTAC 936
 Qy 212 TrpArgLeuAspThrSerArg-----AspGlyTrpHisSerTrpProIleAlaHis 228
 Db 937 TGGCGCTACAGCGAGGCGCGGCGGCCACGACCTCGGTACCTCCTAAGCCCATCACCC--- 993
 Qy 229 GlnTrpProGlnGlyProSerAlaValAspAlaPheSerTrpGluGlu-----Lys 246
 Db 994 GTGTGGAGGCGCATCCACAGGCTCCCCAAGAGGCGCTTCATCAGCAAGGAGGATATTAC 1053
 Qy 247 LeuTyrlleuValGlnGlyThrGlnValTyValPheLeuThrLysGlyTyThrLeu 266
 Db 1054 ACCTATTTCTACAGGCGCGGCGGACTACTGGAAGTTTGACAA----- 1095
 Qy 267 ValSerGlyTyProLysArgLeuGluLysGluValGlyThrProHisGlyIleLeu 286
 Db 1096 -----CAGAACTGAGCGTGAGCGAGGCTACCCGCGCAACATCTCGCT 1140
 Qy 287 AspSerValAspAlaAlaPheIleCysProGlySerSerArgLeuHisIleMetAlaGl 306
 Db 1141 GAC-----TGGATGGGCTGC 1155
 Qy 306 yArgArgLeuTrpTrpLeuAspLeuLysSerGlyVala-----GlnAlaThrTrpThrGl 324
 Db 1156 AACCAAGAGGAGGTGGAGCGCGGAGCGCGGTGCCCCAGGACGAGCGTGGACATC 1215
 Qy 324 u-----LeuProTrpProHisGluLysValas 333
 Db 1216 ATGGTGACCATCAAGATGTCCGGGTCCGTGAACGCGGTGGCGGTGCTCA----- 1267

Score: 183.50 Matches: 60
Percent Similarity: 36.99% Conservative: 31
Best Local Similarity: 24.39% Mismatches: 80
Query Match: 8.40% Indels: 75
DB: 4 Gaps: 10

US-09-900-448-2 (1-391) x US-09-023-655-1040 (1-2223)

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Qy 23 AlaThrProLeuProThrSerAlaHisGlyAsnValAlaGluGlyThrLysPro 42
Db 864 AGCAACCTTCCAACTACT-----GGACCAAGCAGCACCC 899
Qy 43 AspProaspValThrGluArgCysSerAspGlyTrpSerPheAspAla---ThrThrLeu 61
Db 900 AAACCC-----TGTGACCCCGATTGATTTGATGCTATCACCACACTC 944
Qy 62 AspAspAsnGlyThrMetLeuPhePheLysGlyGluPheValTrpLysSerHis----- 79
Db 945 -----CGTGAGAAATACITTTCTTAAGACAGGTACTCTGGAGAGGCATCTCTCAG 998
Qy 80 -----LysTrpAspArgGluLeuIleSerGluArgTrpLysAsnPheProSerProVal 97
Db 999 CTACAAAGATCGAAATGAATTTATTTCTTCTATCTGCGCATCCCTTCCAACTTGGTATA 1058
Qy 98 AspAlaAlaPheArgGln---GlyHisAsnSerValPheLeuIleLysGlyAspLysVal 116
Db 1059 CAGCTCTGATGAGATTTTGAAGATTTGACAGAGACTCTCAATTTCTTATTAAGGCAACCATAC 1118
Qy 117 TrpValTrpProGluLysLysGluLysGlyTrpProLysLeuLeuGlnAsp---Glu 135
Db 1119 TGGGCTCTGAGTGCTATGATATTTCTGCAAGGTTATCCCAAGGATATATCAAACTATGCG 1178
Qy 136 PheProGlyLeuProSerProLeuAspAlaAlaValGluCysHisArgGlyGluCysGln 155
Db 1179 TTCCCCAGCGCTCCAGCAATTTGACGACTGT----- 1214
Qy 156 AlaGluGlyValLeuPhePheGlnGlyHisGlyHisArgAsnGlyThrGlyHisGlyAsn 175
Db 1215 -----TTCTACAGA----- 1223
Qy 176 SerThrHisGlyProGluTyMetArgCysSerProHisLeuValLeuSerAlaLeu 195
Db 1223 ----- 1223
Qy 196 ThrSerAspAsnHisGlyAlaThrTyAlaPheSerGlyThrHisTrpTrpArgLeuAsp 215
Db 1224 -----AGTAAACATACCTCTTTGTAATGACCAATCTGGAGATATGAT 1268
Qy 216 ThrSerArg-----AspGlyTrpHisSerTrpProIleAlaHisGlnTrpProGln 232
Db 1269 AACCAAGACAAATTCATGAGCCAGGTATCCCAAGACATATCAGGTGCGCTTTCCAGGA 1328
Qy 233 GlyProSerAlaValAspAlaAlaPheSerTrpGluGluLysLeuTyLeuValGlnGly 252
Db 1329 ATAGAGATGAAGTGTGAGCGAGTTTTCAGCAAGAACATTTCTTCCATGCTTCAGTGA 1398
Qy 253 ThrGlnValTyValPhe 258
Db 1389 CCAAGATATTAGCATTT 1406
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RESULT 13

US-09-023-655-1410
Sequence 1410, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seihamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-8555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1410:
SEQUENCE CHARACTERISTICS:
LENGTH: 2247 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9456256
US-09-023-655-1410

Alignment Scores: 2,53e-08 Length: 2247
Pred. No.: 183.50 Matches: 85
Score: 30.15% Conservative: 32
Percent Similarity: 21.91% Mismatches: 130
Best Local Similarity: 8.40% Indels: 141
Query Match: 4 Gaps: 20
DB:

US-09-900-448-2 (1-391) x US-09-023-655-1410 (1-2247)

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Qy 13 LeuTrpSerLeuCysTrpSerLeuAlaIleAlaThrProLeuProThrSerAlaHis 32
Db 775 CTATATGGCCAGCCCTGGCCC---ACTGTCACTCCAGGACCCAGCCCTGGGCCCCAG 831
Qy 33 GlyAsnValAlaGluGlyGluThrLysPro---AspProaspValThrGluArgCysSer 51
Db 832 GCTGGGATAGACCAATGAGATTGCACTGCGAGCCAGACGCCCGCCGAGTGCCTGT 891
Qy 52 AspGlyTrpSerPheAspAlaThrThrLeuAspAspAsnGlyThrMetLeuPhePheLys 71
Db 892 GAGGCC---TCCITTGACGGGTCTCC---ACCATCCGAGGCGAGCTCTTTTCTTCAA 945
Qy 72 GlyGluPheValTrpLysSerHisLysTrpAspArgGlu-----LeuIle 86
Db 946 GCGGGCTTTGTGTGGGCGCTCCCGTGGGGGCGAGCTGCGCCGCGCTACCCAGCATTTGCC 1005
Qy 87 SerGluArgTrpLysAsnPheProSerProValAspAlaAlaPheArgGlnGlyHisAsn 106
Db 1006 TCTGCGCACGTGGCAGGACATGCGCCAGCCCTGTGAGAGCTGCTCTTCGAGGATGCCAGGGC 1065
Qy 107 SerValPheLeuIleLysGlyAspLysValTrpValTrpProGluLysLysGluLys 126
Db 1066 CACATTTGGTTCTTCCAAAGGTGCTCAGTACTGGGTGTACGACGGTGAAGAGCCAGTCTGT 1125
Qy 127 GlyTyProLysLeuLeuGlnAspGluPheProGlyIleProSerProLeuAspAlaAla 146
Db 1126 GGC-----CCCGACCCCTTCCCGAGCTG 1149
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QY 147 ValGluCysHisArgGlyGluCysGlnAlaGluValLeuPhePheGlnGlyHisGly 166
Db 1150 -----GGCTGGTGAGGTTCCCGTCCATGCT 1176
QY 167 HisArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGlyProGluTyrMetArgCys 186
Db 1177 -----GCCTTGGTCTGGGGTCCGAG----- 1197
QY 187 SerProHisLeuValLeuSerAlaLeuThrSerAspAsnHisGlyAlaThrTyrAlaPhe 206
Db 1198 -----AGAACACAGATCTACTTCTTC 1218
QY 207 SerGlyThrHisTyrTrpArgLeuAspThrSerArgAspGlyTyrHisSerTrpProle 226
Db 1219 CGAGGACGAGGACTACTGGCGTTTCCACCCACCGCGCGGTAGACAGT---CCCGTG 1275
QY 227 -----AlaHisGlnTrpProGlnGlyProSerAlaValAspAlaAlaPheSerTrp 243
Db 1276 CCCCCAGGCGCACTGACTGGAGGGGTGCCCTCTGAGATGAGCGTCCCTTC----- 1329
QY 244 GluGluLysLeuTyrLeuValGlnGlyThrGlnValTyrValPheLeuThrLysGly--- 262
Db 1330 -----CAGGATGCTGATGGCTATGCTACTTCTCTGGCGCGCGCGC 1368
QY 263 -----GlyTyrThrLeuValSerGlyTyrProLysArgLeu 274
Db 1369 CTCTACTGGAAGTTTGACCCCTGTGAAGGTGAAGGCTCTGGAAGGCTTCCCGCTCTCGTG 1428
QY 275 GluLysGlu-----ValGly 279
Db 1429 GGTCTCTGACTTCTTGGCTGTGCGGAGCTGCGAACACTTCTCTGACCATGGCTTGA 1488
QY 280 ThrProHisGlyLeuLeuLeuAspSerValAspAlaAlaPheLeuCys-----Pro 296
Db 1489 TGCCCTTCAGGG-----TGCGCA----- 1566
QY 297 GlySerSerArgLeuHisIleMetAlaGlyArgArgLeuTrp-----TrpLeuAsp 313
Db 1516 GGC-----CACGAATATCAGGTAGAGACCCATGGCCATCTTTGGGCTG--- 1560
QY 314 LeuLysSerGlyAlaGlnAlaThrTrpThrGluLeuProTrpProHisGluLysValAsp 333
Db 1561 -----TGCGCA----- 1566
QY 334 GlyAlaLeuCysMetGluLysSerLeuGlyProAsnSerCysSerAlaHisGlyProGly 353
Db 1567 -----CCAGCATGGGACTGAGCCCATGTCTCTCGCAGGGGATGG 1608
QY 354 LeuTyrLeuIleHisGlyProAsn 361
Db 1609 GTGGGGTACAAACCATGACAAC 1632

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RESULT 14

US-07-794-393-1

Sequence 1, Application US/07794393

Patent No. 5236844

GENERAL INFORMATION:

APPLICANT: CHAMBER, PIERRE

APPLICANT: BASSET, PAUL

APPLICANT: BELLOCO, JEAN-PIERRE

TITLE OF INVENTION: ANALYTICAL MARKERS FOR MALIGNANT BREAST

TITLE OF INVENTION: CANCER

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox

STREET: 1225 Connecticut Ave. NW Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/794,393

FILING DATE: 19911121

CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: GB 9025326.1

FILING DATE: 21-NOV-1990

ATTORNEY/AGENT INFORMATION:

NAME: GOLDSTEIN, JORGE A

REGISTRATION NUMBER: 29,021

REFERENCE/DOCKET NUMBER: 1383.0040000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 466-0800

TELEFAX: (202) 833-8716

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2256 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: CDS

LOCATION: 10..1473

US-07-794-393-1

Alignment Scores:

Pred. No.:	2,54e-08	Length:	2256
Score:	183.50	Matches:	85
Percent Similarity:	30.15%	Conservative:	32
Best Local Similarity:	21.91%	Mismatches:	130
Query Match:	8.40%	Indels:	141
DB:	1	Gaps:	20

US-09-900-448-2 (1-391) x US-07-794-393-1 (1-2256)

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QY 33 GlyAsnValAlaGluGlyGluThrLysPro---AspProAspValThrGluArgCysSer 51
Db 832 GCTGGGATAGACCAATGAGATTGACCGTGGAGCCAGACGCCGCCGCCAGATCCCTGT 891
QY 52 AspGlyTyrSerPheAspAlaThrThrLeuAspAspAsnGlyThrMetLeuPhePheLys 71
Db 892 GAGGCC---TCCTTTGACGGGTCTCC---ACCATCCGAGGCGAGCTCTTTTCTTCAA 945
QY 72 GlyGluPheValTrpLysSerHisLysTrpAspArgGlu-----LeuIle 86
Db 946 GCGGGCTTTGTGTGGCGCTCCGTGGGGGCCAGCTGCAGCCCGGCTACCCAGCATGGCC 1005
QY 87 SerGluArgTrpLysAsnPheProSerProValAspAlaAlaPheArgGlnGlyHisAsn 106
Db 1006 TCTGGCACTGGCAGGACTGCCAGCCCTGTGGAGCTGCTTCGAGGATGCCAGGCGC 1065
QY 107 SerValPheLeuIleLysGlyAspLysValTrpValTyrProGluLysLysGlyLys 126
Db 1066 CACATTTGGTTCTCCAGGTGCTCAGTACTGGGTGTAGACGCGTCAAAAGCCAGTCTCG 1125
QY 127 GlyTyrProLysLeuLeuGlnAspGluPheProGlyIleProSerProLeuAspAlaAla 146
Db 1126 GGC-----CCGCGACCCCTCCCGAGCTG 1149
QY 147 ValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPhePheGlnGlyHisGly 166
Db 1150 -----GGCTGGTGAGGTTCCCGTCCATGCT 1176
QY 167 HisArgAsnGlyThrGlyHisGlyAsnSerThrHisHisGlyProGluTyrMetArgCys 186

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Qy 244 GluGluLysLeuTyLeuValGlnGlyThrGlnValTyValPheLeuThrLysGly--- 262
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; Sequence 1, Application US/08001711
; Patent No. 5484726
; GENERAL INFORMATION:
; APPLICANT: BASSET, PAUL
; APPLICANT: BELLOCO, JEAN-PIERRE
; APPLICANT: CHAMSON, PIERRE
; TITLE OF INVENTION: ANALYTICAL MARKERS FOR MALIGNANT BREAST
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Suite 300
; CITY: Washington
; STATE: D.C.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/001,711
; FILING DATE: 19930107
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 07/794,393
; FILING DATE: 11-NOV-1991
; PRIOR APPLICATION DATA: GB 9025626.1
; APPLICATION NUMBER:
; FILING DATE: 21-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 1383.0040001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)468-0800
; TELEFAX: (202)833-8716
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2256 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..1473
; US-08-001-711-1
Alignment Scores: 2.54e-08 Length: 2256
Pred. No.: 183.50 Matches: 85
Score: 30.15% Conservative: 32
Percent Similarity: 21.91% Mismatches: 130
Best Local Similarity: 8.40% Indels: 141
Query Match: 1 Gaps: 20
US-09-900-448-2 (1-391) x US-08-001-711-1 (1-2256)
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Db 775 CTATATGCCAGCCCTGGCCC---ACTGTCACTCCAGGACCCCGCCTGGGCCCCCAG 831
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Db 832 GCTGGGATGACACCAATGAGATGTCACCGCTGGAGCCAGCCGCCCGCCAGATGCTGT 891
Qy 52 AspGlyTrpSerPheAspAlaThrThrLeuAspAspAsnGlyThrMetLeuPheLys 71
Db 892 GAGGCC---TCCCTTGGACGGGTCTCC---ACCATCCGAGGCGAGCTCTTTCTTCAA 945
Qy 72 GlyGluPheValTrpLysSerHisLysTrpAspArgGlu-----Leulle 86
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Qy 147 ValGluCysHisArgGlyGluCysGlnAlaGluGlyValLeuPhePheGlnGlyHisGly 166
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Db 1177 -----GCCTTGGTCTGGGTCCCGAG----- 1197
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1489	DB	TGCCCTCAGGG-----TGCTGACCCCTGCCCA 1515	
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334	QY	GlyAlaLeuCysMetGluLysSerLeuGlyProAsnSerCysSerAlaAsnGlyProGly	353
1567	DB	-----CCAGGCATGGGACTAGCCCATGTCTCTCTGACGGGGGATGGG 1608	
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1609	DB	GTGGGGTACAACCAACCATGACAAC 1632	

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Job time : 109 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2004, 18:54:10 ; Search time 829.5 Seconds
(without alignments)

16499.081 Million cell updates/sec

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Perfect score: 3000

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2395936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:**

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1509.4	50.3	5234	15	US-10-311-455-917
3	1281.6	42.7	5234	15	US-10-311-455-918
4	147	4.9	384	10	US-09-918-995-7738
5	130	4.3	422	10	US-09-918-995-8595
6	130	4.3	488	10	US-09-918-995-30828
7	130	4.3	1631	15	US-10-125-237-19
8	130	4.3	1631	15	US-10-105-891-19
9	130	4.3	3186	11	US-09-900-448-1
10	128.4	4.3	492	10	US-09-918-995-31395
11	94.8	3.2	225	9	US-09-960-352-3470
12	94.8	3.2	237	9	US-09-960-352-7532
13	94.8	3.2	373	9	US-09-960-352-2026
14	94.8	3.2	384	9	US-09-960-352-9132

ALIGNMENTS

RESULT 1

US-09-900-448-3
; Sequence 3, Application US/09900448
; Publication No. US20030220488A1

; GENERAL INFORMATION:

; APPLICANT: CECARDI, Toni et al.

; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,

; NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: CLO01272

; CURRENT APPLICATION NUMBER: US/09/900,448

; CURRENT FILING DATE: 2001-07-09

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 13737

; TYPE: DNA

; ORGANISM: Human

; US-09-900-448-3

Query Match 100.0%; Score 3000; DB 11; Length 13737;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	121	TAGGTTTCAGAGGCTCAGAGGAGGAAGAAAGGTGAGGGGAGTCTTAGAATAGTGCTC	180
Db	121	TAGGTTTCAGAGGCTCAGAGGAGGAAGAAAGGTGAGGGGAGTCTTAGAATAGTGCTC	180
Qy	181	CCATTGCCAACACCCAGAAAGAGACATCCCTGCAATGGGAGAGGTCATGATGAGA	240

Sequence 4209, Ap
Sequence 8898, Ap
Sequence 4643, Ap
Sequence 457, App
Sequence 7514, Ap
Sequence 445, App
Sequence 2956, Ap
Sequence 136, App
Sequence 6107, Ap
Sequence 5619, Ap
Sequence 2507, Ap
Sequence 8662, Ap
Sequence 14176, A
Sequence 13395, A
Sequence 7056, Ap
Sequence 3702, Ap
Sequence 9378, Ap
Sequence 380, App
Sequence 13402, A
Sequence 431, App
Sequence 5920, Ap
Sequence 7025, Ap
Sequence 7320, Ap
Sequence 6078, Ap
Sequence 87, Appl
Sequence 1789, Ap
Sequence 13635, A
Sequence 8017, Ap
Sequence 14603, A
Sequence 84, Appl
Sequence 39, Appl

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1742 |||||
1743 CTTCAGCAGTGTAGCCAGTTACTGCTTGAATTTGTGAAAGGGGTTGGGGGCGAGCTG 1800
1744 |||||
1801 CCGGGAAGAGGAGTCTTGATTCAGATTTCTGTCAGACCCCTGACCTTATTTTGGAGTGA 1860
1802 |||||
1803 CCGGGAAGAGGAGTCTTGATTCAGATTTCTGTCAGACCCCTGACCTTATTTTGGAGTGA 1860
1804 |||||
1861 TGTAAATCAGCAATATTTGCTTGTAGTCTGAGAGACAGCAATTCCTCAGTAGAGTTGGAGG 1920
1862 |||||
1863 TGTAAATCAGCAATATTTGCTTGTAGTCTGAGAGACAGCAATTCCTCAGTAGAGTTGGAGG 1920
1864 |||||
1921 TGGGGGTGTGTGCTGCTGCAACTTATATAGGAGGTTCACTGCTCACCAGCAGCTGCTC 1980
1922 |||||
1923 TGGGGGTGTGTGCTGCTGCAACTTATATAGGAGGTTCACTGCTCACCAGCAGCTGCTC 1980
1924 |||||
1981 TGTGGCTCTCTGACGCTCAGCATGCTAGGTTAGGTTAGGAGCAGCCCTTGCACCTGGGGTTGT 2040
1982 |||||
1983 TGTGGCTCTCTGACGCTCAGCATGCTAGGTTAGGTTAGGAGCAGCCCTTGCACCTGGGGTTGT 2040
1984 |||||
2041 GGGCTCTATGCTGCTCTGCGCATTTGCCACCTCTTCTCCTCGTCAAGTAAAGCTGGGAC 2100
2042 |||||
2043 GGGCTCTATGCTGCTCTGCGCATTTGCCACCTCTTCTCCTCGTCAAGTAAAGCTGGGAC 2100
2044 |||||
2101 TAGAAGCGAAGGATTCAGTTCTGGGCTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTT 2160
2102 |||||
2103 TAGAAGCGAAGGATTCAGTTCTGGGCTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTT 2160
2104 |||||
2161 CAAATTTGGGGTCAGGGCTATGAGGAAAGGATTCGGTCCCAATGAGTCAAGTATCTAT 2220
2162 |||||
2163 CAAATTTGGGGTCAGGGCTATGAGGAAAGGATTCGGTCCCAATGAGTCAAGTATCTAT 2220
2164 |||||
2221 TTGCTCTCCTAGGACTAGTGGCCATGCGGAAATGTTCTGAAAGCGAGACCAAGCCAGACC 2280
2222 |||||
2223 TTGCTCTCCTAGGACTAGTGGCCATGCGGAAATGTTCTGAAAGCGAGACCAAGCCAGACC 2280
2224 |||||
2281 CAGACGTGACTGGTGGGCTGAGCTCCCTAAAGTCTCTATCTCTCTGTTGTTCTCTC 2340
2282 |||||
2283 CAGACGTGACTGGTGGGCTGAGCTCCCTAAAGTCTCTATCTCTCTGTTGTTCTCTC 2340
2284 |||||
2341 TGCATTTTATCAGCTTCTGGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCT 2400
2342 |||||
2343 TGCATTTTATCAGCTTCTGGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCT 2400
2344 |||||


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QY 2401 ACCTCCACCCAGACCGCTGCTCAGATGGCTGGAGCTTTGATGCTACCAACCTCGGATGAC 2460
DB 2401 ACCTCCACCCAGACCGCTGCTCAGATGGCTGGAGCTTTGATGCTACCAACCTCGGATGAC 2460
QY 2461 AATGGAACCATGCTGTTTTTAAAGGTAGAGGACTGAGGCTTAGGGCGTTTAGGACCTT 2520
DB 2461 AATGGAACCATGCTGTTTTTAAAGGTAGAGGACTGAGGCTTAGGGCGTTTAGGACCTT 2520
QY 2521 AGACTTACTCTCTCTTCAAAAGGGTGTCCCTGCTGTGTGGAGGCTTAGGAATTAATCTGA 2580
DB 2521 AGACTTACTCTCTTCAAAAGGGTGTCCCTGCTGTGTGGAGGCTTAGGAATTAATCTGA 2580
QY 2581 TGGTATCACTGACAGCTTCTCTCAAGCTATCTCAGTAGTCAAGGTTTCTCACTGGGCC 2640
DB 2581 TGGTATCACTGACAGCTTCTCTCAAGCTATCTCAGTAGTCAAGGTTTCTCACTGGGCC 2640
QY 2641 CTTCACTGAGTGTGGTTTTTCAAGGGAGTTTGTGTGGAAGAGTCAAAATGGGACCGG 2700
DB 2641 CTTCACTGAGTGTGGTTTTTCAAGGGAGTTTGTGTGGAAGAGTCAAAATGGGACCGG 2700
QY 2701 GAGTAAATCTCAGAGAGTGGAGAAATTTCCAGCCCTGTGGATGCTGCTATTCCTCAA 2760
DB 2701 GAGTAAATCTCAGAGAGTGGAGAAATTTCCAGCCCTGTGGATGCTGCTATTCCTCAA 2760
QY 2761 GGTCAACAGTGTCTTCTGATCAAGGTACTGCTGGGCCCAAAATCAGGGCCAGGCTGGA 2820
DB 2761 GGTCAACAGTGTCTTCTGATCAAGGTACTGCTGGGCCCAAAATCAGGGCCAGGCTGGA 2820
QY 2821 AAGGCTGGAATCGACACTGGGAGACCTTCCCAAAATGGCCCTTGGCATGGAGCCCATAG 2880
DB 2821 AAGGCTGGAATCGACACTGGGAGACCTTCCCAAAATGGCCCTTGGCATGGAGCCCATAG 2880
QY 2881 CAATAGGTAGCAGATTTCTTCCCAATGTCCTCTTCTCTGTAAGCTTGGGCTAAGG 2940
DB 2881 CAATAGGTAGCAGATTTCTTCCCAATGTCCTCTTCTCTGTAAGCTTGGGCTAAGG 2940
QY 2941 GAGTGTGATGCTGTGGGCTTGGAGTGCACCATCCAGTGGCTGTTCTTCAGTCTAG 3000
DB 2941 GAGTGTGATGCTGTGGGCTTGGAGTGCACCATCCAGTGGCTGTTCTTCAGTCTAG 3000
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RESULT 2

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US-10-311-455-917
; Sequence 917, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEX, Alexander
; APPLICANT: PISENBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 917
; LENGTH: 5234
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
US-10-311-455-917
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Query Match 50.3%; Score 1509.4; DB 15; Length 5234;
Best Local Similarity 79.9%; Pred. No. 0;
Matches 1777; Conservative 0; Mismatches 446; Indels 0; Gaps 0;
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QY 12 AGGAGGCCCCAGCMAAATCTGTAGGATTCAGACAGGGTTCTGACAGCTGACAGCAAGTTG 71
DB 3012 AGGTAGGTTTGTAGTAAATTTGTAGGATTTAGTAGGGTTTGTATAGTGTGAAGTAAAGTTG 3071
QY 72 TTGAGGAAATTCCTGATGAGGATCATGGGGTCTCAGGAGGAGAAATATAGGTTTTCAG 131
DB 3072 TTGAGGAAATTTTGTGATGAGGATTTATGGGGTGTTAGGAGGAGAAATATAGGTTTTCAG 3131
QY 132 AGGCTGACAGGAAAGAAAGGTGAGGGGAGTCTTAGAAATAGTGGCTCCCATTCGCCAA 191
DB 3132 AGGTTGACAGGAAAGAAAGGTGAGGGGAGTCTTAGAAATAGTGGCTCCCATTCGCCAA 3191
QY 192 CACCCAGAAAGAGACATGCCCTGCAATGGGAGAGAGTGTAGTATGACACATTTGGCTGTA 251
DB 3192 TATTTAGAAAGAGATATGTTTTGTATGGGAGAGAGTGTAGATATTTGGTTGTA 3251
QY 252 GCAGCGATGGCATTTGCCAGGCTGCCAAGGACTCAGAGAGTCCAGGCTTGGCCACTGACC 311
DB 3252 GTAGCGATGGTATTTGTTTAGGTTGTTTAGGATTTTAGAGAGTTTAGTTTGTATTGATT 3311
QY 312 TATGAGGAGGAGATGATGTTTACAGCACATTTTATGCTAGTCCAGGAGGACATTTGA 371
DB 3312 TATGAGGAGGAGATGATGTTTATAGTATATTTTATTCGTAAGTATGAGAGGATATTTGA 3371
QY 372 CCCTGATGCGACAGGCGCTGCTGACATGTTTTCAGAGGTTCCGGAATGTGTTTCT 431
DB 3372 GTTTGATGAGAGTTTGGTGATATGTTTGTAGAGTTTCGGAATGTGTTTCT 3431
QY 432 GTTGAAGGAAATCTTGGCAGAGTGAAGAGGATCTGAGACTTTTGGTAAGTATATAT 491
DB 3432 GTTGAAGGAAATTTCTGAGAGTGAAGAGGATTTGAGATTTTGGTAAGTATATAT 3491
QY 492 GGGAGTGTGAGGCTTGGGACCATCTGAGGAGTCAAGGCGCTTTCAGGCTTGGCTAG 551
DB 3492 GGGATGTTTGGGGTTTGGAGTATTTGTGAGGAGTATGGGTTTTTTAGTTTGGTTAG 3551
QY 552 GGAGCAGGGTCTCGGAATTTTATCTGCGCCATAGCTGCTGCCATATTTCTTTTC 611
DB 3552 GGAGTAGGGTTTTTGGAAATTTTATTTGGTTTATAGTTAGTTTGTATATATTTT 3611
QY 612 TGACTCTAGGCAAAATCTCACACAAATGGGCGAGCTTTGGAGTGGGCCCGAGGT 671
DB 3612 TGATTTATAGGTAAATTTTATATAGAAATGGGGTAGTTTGGAGTGGGTTTAGGAGT 3671
QY 672 ACTGAGATAGCTGAGATCCAGGAGAGATGAGTGTGGGGCCGAGACACTGAGAG 731
DB 3672 ATTGAGGATAGTGTGAGATTTTAGGAGAGATGAGTGTGGGTCGAGATATTTGAGAG 3731
QY 732 AGAAACAGGACTGTCAGATAAAGGGCGTCTGTGACTCTCTAGATCTCATTTGCTACTAC 791
DB 3732 AGAAATAGGATTTGTAGATAAAGGGCGTCTGTGATTTTATAGATTTTATTTATTTAT 3791
QY 792 CATAACCTACCCCAATTTCTTAATTTCTCTACCTAGAGGGGGGAAATTTGTCAGAAA 851
DB 3792 TATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 3851
QY 852 TTTGGCTGCAACACTAGCACACTCTCAGTACTTGAATGCAATTTTGTCAATTTTTC 911
DB 3852 TTTGGTGTAAATATTTAGTAAATATTTATTTAGTATTTGAATTTTATTTTATTTTATTT 3911
QY 912 TTCAACAATATTTCTGGAACACTCTTATATGCGGCACTATTTTATGAGTCTAGGAT 971
DB 3912 TTTAATAATATTTTCTGGAATATTTTATATGTTAGTATTTTATTTAGGAGTTAGGAT 3971
QY 972 ATATAATGTAACAGACAGGCAAAACAAAGCAAGCAACCAACCAACCATCACAGATA 1031
DB 3972 ATATAATGTAACAGATAGGTAAATAAAGTAAAGTAAATAATATTAATTTATTTAGATA 4031
QY 1032 GTAGACAGATGAAGAGATTTCAAGTTTTTGTAGTAAATAAACAACAGGCTCTGAA 1091
DB 4032 GTAGATAGTGAAGAGATTTTAAAGTTTTTGTAGTAAATAAATAAAGTAAAGGTTTGA 4091
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Qy	1092	ATGCTAGATAAGCGGTC	CAAGAAAGGCTTCATTAGAGAGGTAGCATTTAAGCAGGAGTC	1151
Db	4092	ATGGTTAGATAAGGTGGT	TAAAGAAAGGTTTTATTAGAGAGGTAGTATTATTAGTAGTAGGAGTT	4151
Qy	1152	AGCTAGAAATATGTGAAAT	TCAGATTCAGTTCATATTGGTCTCGGTTGGTGGTAAATAA	1211
Db	4152	AGTTAGAAATATGTGAAAT	TTTAGTTAGTGTATTATTGTTTGGGTTGGTGGTAAATAA	4211
Qy	1212	GCTTTTTCCCCAAGGTGGAA	CACTACCAAGAAAGCTAAATTACTAGTAGTGGTGGCTC	1271
Db	4212	GTTTTTTTTTTAAAGTGGA	AAATATTAAAGAAAGATTAAATTAATTAGTAGTGGTGGTGT	4271
Qy	1272	TCTCGAGAGAGACACCTC	CTGTTCCTGCCTCATTACTGTCACACCCCTCACTCCAGGCA	1331
Db	4272	TTTCGAGAGAGATATTTTT	TGTTTTGTTTTATTATTTGTTTTATTATTTGTTTATTTTTTAGGTA	4331
Qy	1332	CTTTTTGCAAAAGCCCTT	TGCCAGTCAGGAAAGGCGAGAGGCTGGGCATGGGCGCTGGACA	1391
Db	4332	TTTTTTGTAAAGTTTTT	TGTAGTTAGGTAAGGCGAGAGGTTGGGTATGGGTTTTGGATA	4391
Qy	1392	TTTCACACACTGTGACAT	TAATTGTTCCCGACACTCACTAGCCCAAGGGTAAAGCTGAGGA	1451
Db	4392	TTTGATAATAGTGAGATA	TATTTGTTTTTAGATTATTACTAGTTTAAAGGGTAAAGTTGAAGA	4451
Qy	1452	GGCTTGGGCATGCCCGA	AGAGGCCCTGATGAAGAGCTGGAAAAAGCTGTCTCTGAGTA	1511
Db	4452	GGTTGGGTATGTTTTAG	AAAGGTTTTGATGAAGTTTGGAAAAAGTTGTTTTTTGAGTA	4511
Qy	1512	TTTCTAGTAAGTTTATCT	GTGTGTGTGGTTACTAAAGTAGTAGTAATTTGCTGTCTCTA	1571
Db	4512	TTTTTAAAGTAAGTTTAT	TGTGTGTGGTTTATTAAAAAGTAGTAGTAATTTGTTGTTTTTA	4571
Qy	1572	GCTGCTTTAGACGAGGCT	TCACACAGTACAGCAATATTAGTTCCCTCTCTTTTCTCAC	1631
Db	4572	GTGTGTTTTAGAGTAGG	TTTGATATAGTAATATTAGTTTTTTTTTTTTTTTTTTTTTAT	4631
Qy	1632	CTCCCCAATTGTGAGATA	AAACTCAATCACAAAAGGTGATCCTCAGTCTACTCCTCTCCC	1691
Db	4632	TTTTTTTTTTGTGAGATA	AAATTTAAATATAAAAGGTCATTTTTTAGTTTATTATTATTTTTT	4691
Qy	1692	TGACTTATGAGTCTGAG	CCATTGCCAGTGTGAGAGTCACAGCTGGAGCTGACGAGTG	1751
Db	4692	TGATTTATGATGTGTG	ATTTATTTAGTGTGAGAGTTATAGTTGCACTGTAGTAGTG	4751
Qy	1752	TAGCCCACTTACTGCTT	GAAATTTGCTGAAGGGGGTTGGGGGGCAGCTGCCGGGAAAAAG	1811
Db	4752	TAGTTTAGTTATTGTTT	GAAATTTGTTGAAGGGGTTGGGGGGTAGTTGTCGGGAAAAAG	4811
Qy	1812	GAGTCTTGGATTAGATT	CTGTCCAGACCTGACCTTATTGTCAGTGTATGTATATGAGCC	1871
Db	4812	GAGTTTTGGATTAGATT	TTTTTTTGTAGATTTTGATTTTATTATTGTTAGTGATGTAAATAGTT	4871
Qy	1872	AATATTGGCTTAGTCT	CTGGGAGACGACATTCACAGTAGAGTTTGGAGGTTGGGGGCTGGTG	1931
Db	4872	AATATTGGTTTTAGTT	TTTGGGAGATGATATTTTTTAGTAGAGTTTGGAGGTGGGGGCTGGTG	4931
Qy	1932	CTGCTGCCAATCTATAT	GAGGAGTTCAACTGGTTCACCCAGAGCTGTCCCTGTGAGCCCTCTG	1991
Db	4932	TTGTGTGTAATTTTATA	PAGGAGTTTAAATTTGGTTATTTAGAGTTGTTTTGTTGTTTTTTG	4991
Qy	1992	CAGCTCAGCATGGCTAG	GGTACTGGGAGCACCCCTTGCACTGGGGTTGTGGAGCCTATGCG	2051
Db	4992	TAGTTTAGTATGTTTAG	GTATTGGGAGTATTGGTGTATTGGGTTTGTGGAGTTTATGT	5051
Qy	2052	TGTTCTCTGGCCATTTG	CCACCCCTCTCTCCGTGTAGTAAAGCTGGGAGCTAGAAAGCGAAG	2111
Db	5052	TGGTTTTTGGTTATTTG	TATTTTTTTTTTTTGTGAGTAAAGTTGGGATTTAGAAAGCGAAG	5111
Qy	2112	GATTGAGTTCTGGGCTA	GGGTAAAGTAGGGCACTTTTTTAGGCTCCGTCAAAATTTTGGGG	2171
Db	5112	GATTGAGTTTGGTTAGG	TGAGGTAGGTTTATGTTTTTTTAGGTTTCGGTTAAATTTGGGG	5171
Qy	2172	TCAGGGGCTATGGGAA	AGGGATCGGTCACCAATGGATCAAGATATCTATTTGTTCTCCCT	2231

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Db      5172 TTAGGGGTATGCGAAAGGCATCGTTTAAATGATTAGATATTTATTGTTTTTTT 5231
Qy      2232 AGG 2234
Db      5232 AGG 5234

RESULT 3
US-10-311-455-918/c
; Sequence 918, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 918
; LENGTH: 5234
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-918

Query Match          42.7%; Score 1281.6; DB 15; Length 5234;
Best Local Similarity 73.4%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches 594; Indels 0; Gaps 0;

Qy      1 TCCCTCTCCCAGCAGGCCCGACCAAAATCTGTAGGATTCAGACAGGGTCTTCACAGCTG 60
Db      2234 TCCCTCTCCCAGCAGGCCCGACCAAAATCTATAAAATCTATAAAATCTAACAAAATCTAACAACTA 2175

Qy      61 AAGACAAGTTGTTTGAGGAATTCCTGATGAGGATCATGGGGTCTCAGAGAGGAGAATA 120
Db      2174 AAAACAATTTATAAAAAATTCCTATAAAAAATCATAAATTAATAAAAAAAAAATA 2115

Qy      121 TAGGTTTCAGAGCTGAGGGGAAGAAAGGTGAGGGGAGCTCTTAGNATAGTGGCTC 180
Db      2114 TAAATTTCAAATCTAAATAAAAAAAAAAAAAATAAAAAAAATCTTAAATTAATAACTC 2055

Qy      181 CCATTGCCCAACACCAGAGAAAGACATGCCCTGCAATGGGAGAGGTGAGTATGAGA 240
Db      2054 CCATTACCCACACCCCAAAAAAACAATACCTCAATAAAAAAATAAATAATAAAA 1995

Qy      241 CATTTGGCTFAGAGCGATGGCTTCGCCCGCTGCCAAGGACTCAGAGAGTCCAGCCTT 300
Db      1994 CATTAACTATAACACGATAACATTAACCCAACTACCAAAATCTAAAAAATCCAACCTT 1935

Qy      301 GCCCACTGACCTATGAGGAGGGAATCATGTTCAACAGCAATTTTCATTGGTAGTCAGGA 360
Db      1934 ACCCACTAACCTATAAAAAAATAAATAATTCACAACAATTTTCATTGGTAAATCAAAA 1875

Qy      361 GAGGACATTTAGCGCTGATGGCAGAGCGCTGGTGACATATGTTGTCAGAGGTTCCGGAATG 420
Db      1874 AAAAAACATTTAAACCTAATAACAAAAACCTTAATAACAATATTATTTCAAAAAATTCGAAATA 1815

Qy      421 TGTTGTTTCTCTGTTGGAAGAACTTCGCAGAGTAGAAGGAGATCTCGAGACTTTTGGTA 480
Db      1814 TATATTTTCTTATTAATAAAAAAACTTCGCAATAATAAAAAAANAATCTAAACTTTTAATA 1755

Qy      481 AGATATATATGGAAGCTGTACAGGGGTCTGGAGCCATCTGTGAGGGATCAAGGCCCTTTCA 540

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Db 1754 AAATATATATAAATCTATCAAAAATCTAAACCATCTATAAAAAATCAAAACCCCTTTCA 1695
Qy 541 GCCTTGCTAGGAGCAGGAGGCTCTGCAATCTCATCTGCGCCCATAGCTGAGTCTGCCCA 600
Db 1694 ACCTTAACATAAACAAGAAATCTTAACCTCTCATCTACCCCACTAAATCTACCCA 1635
Qy 601 TAATCTCTTCTGACTCACTAGGCAATCTCACACAGAAATGGGGAGCTTTGGGAGTGG 660
Db 1634 TAATCTCTTCTGACTCACTAGGCAATCTCACACAGAAATGGGGAGCTTTGGGAGTGG 1575
Qy 661 GCCAGGAGTCTAGGATAGAGAGTGGATCCCGAGAGAGATGATGCTGGGGCGAG 720
Db 1574 ACCCAAAAATACTATAAATAAACAATAAATCCCAAAAAATAAATAAACAACCGAA 1515
Qy 721 AACTGGAGAGAGAAACAGAGCTGTACAGATAAAGGGGCTGTGCACTCTCTAGATCTCAT 780
Db 1514 AACTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1455
Qy 781 ATGCTACTACCTAATCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTAC 840
Db 1454 ATACCTACTACCTAATCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT 1395
Qy 841 ATTGTGAGAAATTTGGCTGCAACACACTAGCAACACTACTCAGTACTCTGAAATGCAATTT 900
Db 1394 ATTATCAAAATTTTACTACACACTAACAACACTACTCAGTACTCTGAAATGCAATTT 1335
Qy 901 CATTTTCTCAATCAACAAATATTTCTGGACAACTCTTATATGCGAGGCACTATTTAG 960
Db 1334 CATTTTCTCAATCAACAAATATTTCTGGACAACTCTTATATGCGAGGCACTATTTAG 1275
Qy 961 GAGTCAGGGATATATATGTAACAAGACAGGCAACAAACAAACAAACAAACAAACAAAC 1020
Db 1274 AATCAAAAT 1215
Qy 1021 TCACACAGATAGTAGACAGATGAAGAAATTTCAAGTTTATAGTAGTAAATATAAACAAGC 1080
Db 1214 TCACCAATATAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1155
Qy 1081 AAGGCTGTAATGCTAGTAGAGCGGTCAAGAAAGCTTCTATGAGAGAGTGAAGTATTT 1140
Db 1154 AAAATCTAAATTAACATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1095
Qy 1141 AAGCAGAGTCAAGTATAGAAATTTGTAATTTCAAGTTTCAAGTTTCAAGTTTCAAGTT 1200
Db 1094 AACAAATCACTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1035
Qy 1201 GGTAAATAAAGCTTTTCCCAAGGTGGAACTACACAGAAAGACTAATTAAGTAGTAG 1260
Db 1034 AATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 975
Qy 1261 TGGTGGTCTCTGGAAGAGAGACACTCTCTGTTCTGCTCTCAATTAAGTCAACCTTC 1320
Db 974 TAATAATCTCTTAAAAAATAAACAACCTCTATTTCTACTCTATTAAGTCAACCTTC 915
Qy 1321 ACTTCCAGGCACTTTTGCAGAGCCCTTTGCGAGTCAAGGAGGCGAGAGCTGGGATG 1380
Db 914 ACTTCCAGGCACTTTTGCAGAGCCCTTTGCGAGTCAAGGAGGCGAGAGCTGGGATG 855
Qy 1381 GGGCTTGACATTTGACACAGTGAAGCATTTATGTCGCCAGAGCTCACTAGCCCAAGGT 1440
Db 854 AAACCTTAACATTTTAAACAAATATAAATATTTATCCCAAGTCACTACCCCAAAAT 795
Qy 1441 AAAGCTGAAGAGGCTTGGGCAATGCCCCAGAAAGGCCCTGATGAAGCTTGGAAAAAGCTG 1500
Db 794 AAACCTTAACATTTTAAACAAATATAAATATTTATCCCAAGTCACTACCCCAAAAT 735
Qy 1501 TTCTCTGATTAATTTCTAGTAAATTTATCTCTGTTGTTGTTCTTAAAGTAGTAAGTAT 1560
Db 734 TTCTCTAATAATTTTCTAATAAATTTATCTATATATATAAATTTCTAATAAATAAATAT 675
Qy 1561 TGCTGTCTCTAGCTGCTCTAGGAGGAGGCTTGACACAGTACACAGCATATTAAGTCTCC 1620

Db 674 TACTATCTCTAATCTACCTTAAAAACAACAACTTAACACATATACACAAATTAATTTCCCT 615
Qy 1621 CTTTTTCTCACTCCCTCCCAATTTGAGAGATAAATCTAATCAAAAAGTGTATCTCTAGTCT 1680
Db 614 CTTTTTCTCACTCCCTCCCAATTTAATAAATAAATAAATAAATAAATAAATAAATAAATA 555
Qy 1681 ACTCACTTCCCTGACTTATGAGTGGCTGACCCATTTGCCAGTGTGAGAGTCAACAGCTGA 1740
Db 554 ACTCACTTCCCTGACTTATGAGTGGCTGACCCATTTGCCAGTGTGAGAGTCAACAGCTGA 495
Qy 1741 CTTCAAGCAGTGTAGCCAGTCTTACTGCTGAAATTTGCTGAAGGGGTTGGGGGAGCTG 1800
Db 494 CGTCAACATATAAACCCTTACTTCTTAAATTTACTTAAATTTACTTAAATTTTAAAAACA 435
Qy 1801 CCGGGAAGAGAGTCTTGGATTCAGATTTCTGTCAGAGCCCTGACCTTATTTGCAAGTGA 1860
Db 434 CCGAAAAAATAAATCTTAAATTTCAAAATTTCTATCCAAACCCCTTAACTTATTTTCAATA 375
Qy 1861 TGTAAATCAGCCCAATATTTGGCTTAGTCTCTGGGAGACAGACATTTCCAGTAGAGTTGGAGG 1920
Db 374 TATAATCAACCAATATTAACCTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATA 315
Qy 1921 TGGGGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Db 314 TAAAAATAAATACTACTACCACTCTATATAAATAAATAAATAAATAAATAAATAAATA 255
Qy 1981 TGTGGCTCTGAGCTCAGCATGGCTAGGCTACTGGGAGCACCCCTTGCACCTGGGTTGT 2040
Db 254 TATACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 195
Qy 2041 GGAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
Db 194 AAAACCTATATAATCTTAAACCAATTTACCACCCCTCTTCTCTCGTAAATAAATAAATA 135
Qy 2101 TAGAGGAGAGGATTCAGTCTGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCTAGGCT 2160
Db 134 TAAAAAGGAGAGGATTTAAATTTCTTAAATTTAAATTTAAATTTAAATTTAAATTTAA 75
Qy 2161 CAAATTTGGGCTCAGGGCTGATGGGAAAGGATTCGGTCCCAATGGATCAAGATATCTATT 2220
Db 74 CAAATTTAAATCAAAAACTTATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 15
Qy 2221 TTGTTCTCCCTA 2232
Db 14 TTATTTCTCCCTA 3

RESULT 4

US-09-918-995-7738
; Sequence 7738, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7738
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-7738

Query Match 4.9%; Score 147; DB 10; Length 384;
Best Local Similarity 100.0%; Pred. No. 2.7e-32;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1985 GCCTCTGCTCAGCTCAGCATGGCTAGGCTGCTGGGAGCACCCGTTGCACTGGGGTTGTGGAG 2044

Db 1 GGCCTGACGCTCAGCATGCTAGGTTACTGGGAGCACCGCTGCACTGGGGTTGTGGAG 60
QY 2045 CTTATGCTGCTCTGCGCCATTGCCACCCCTCTTCTCGTGAAGTAAAGCTGGACTAGA 2104
Db 61 CTTATGCTGCTCTGCGCCATTGCCACCCCTCTTCTCGTGAAGTAAAGCTGGACTAGA 120
QY 2105 AGCGAAGGATTGAGTTCTGGGCTAGGG 2131
Db 121 AGCGAAGGATTGAGTTCTGGGCTAGGG 147

RESULT 5

US-09-918-995-8595
; Sequence 8595, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8595
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-8595

Query Match 4.3%; Score 130; DB 10; Length 422;
Best Local Similarity 96.4%; Pred. No. 3.1e-27;
Matches 133; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2651 TGTGGGTTTTTTCAGGGAGTTTGTGGAAGAGTCACAAATGGGACCGGGAGTTAATCT 2710
Db 213 TGTGTTTTTTTAAAGGGAGTTTGTGGAAGAGTCACAAATGGGACCGGGAGTTAATCT 272
QY 2711 CAGAGATGGAAGAATTTCCCGAGCCCTGTGGATGCTGATTCCTCAAGTCAACA 2770
Db 273 CAGAGATGGAAGAATTTCCCGAGCCCTGTGGATGCTGATTCCTCAAGTCAACA 332
QY 2771 GTGCTTTCTGATCAAGG 2788
Db 333 GTGCTTTCTGATCAAGG 350

RESULT 6

US-09-918-995-30828
; Sequence 30828, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30828
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(488)
; OTHER INFORMATION: n = A,T,C or G

US-09-918-995-30828

Query Match 4.3%; Score 130; DB 10; Length 488;
Best Local Similarity 96.4%; Pred. No. 3.5e-27;
Matches 133; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2651 TGTGGGTTTTTTCAGGGAGTTTGTGGAAGAGTCACAAATGGGACCGGGAGTTAATCT 2710
Db 270 TGTGTTTTTTTAAAGGGAGTTTGTGGAAGAGTCACAAATGGGACCGGGAGTTAATCT 329
QY 2711 CAGAGATGGAAGAATTTCCCGAGCCCTGTGGATGCTGATTCCTCAAGTCAACA 2770
Db 330 CAGAGATGGAAGAATTTCCCGAGCCCTGTGGATGCTGATTCCTCAAGTCAACA 389
QY 2771 GTGCTTTCTGATCAAGG 2788
Db 390 GTGCTTTCTGATCAAGG 407

RESULT 7

US-10-125-237-19
; Sequence 19, Application US/10125237
; Publication No. US20030022329A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhang, Jie
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NO. US20030022329A1el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; FILE REFERENCE: 791CIP2ADIV
; CURRENT APPLICATION NUMBER: US/10/125,237
; CURRENT FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 09/668,317
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/552,929
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 19
; LENGTH: 1631
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (71)...(1459)
US-10-125-237-19

Query Match 4.3%; Score 130; DB 15; Length 1631;
Best Local Similarity 96.4%; Pred. No. 8.1e-27;
Matches 133; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2651 TGTGGGTTTTTTCAGGGAGTTTGTGGAAGAGTCACAAATGGGACCGGGAGTTAATCT 2710
Db 270 TGTGTTTTTTTAAAGGGAGTTTGTGGAAGAGTCACAAATGGGACCGGGAGTTAATCT 329
QY 2711 CAGAGATGGAAGAATTTCCCGAGCCCTGTGGATGCTGATTCCTCAAGTCAACA 2770
Db 330 CAGAGATGGAAGAATTTCCCGAGCCCTGTGGATGCTGATTCCTCAAGTCAACA 389
QY 2771 GTGCTTTCTGATCAAGG 2788
Db 390 GTGCTTTCTGATCAAGG 407

RESULT 8

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US-10-105-891-19
; Sequence 19, Application US/10105891
; Publication No. US20030073099A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhang, Jie
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NO. US20030073099A1el Nucleic Acids and
; FILE REFERENCE: 79ICIP2A
; CURRENT APPLICATION NUMBER: US/10/105,891
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/668,317
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/552,929
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: pt_FJ_genes Version 2.0
; SEQ ID NO 19
; LENGTH: 1631
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (71)..(1459)
US-10-105-891-19

Query Match 4.3%; Score 130; DB 15; Length 1631;
Best Local Similarity 96.4%; Pred. No. 8.1e-27;
Matches 133; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2651 TGTGGTGTTCAGGGAGTTTGTGGAAGAGTCACAAATGGGACCGGAGTTAACT 2710
DB 270 TGCTGTGTTCAGGGAGTTTGTGGAAGAGTCACAAATGGGACCGGAGTTAACT 329
QY 2711 CAGAGATGGAAGATTTCACCCAGCCCTGTGGATGCTGCATTCGTCAGGTCAACA 2770
DB 330 CAGAGATGGAAGATTTCACCCAGCCCTGTGGATGCTGCATTCGTCAGGTCAACA 389
QY 2771 GTGCTTTCTGATCAAGG 2788
DB 390 GTGCTTTCTGATCAAGG 407

RESULT 9
US-09-900-448-1
; Sequence 1, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
; APPLICANT: CECCARDI, Toni et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; FILE REFERENCE: CL001272
; CURRENT APPLICATION NUMBER: US/09/900,448
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3186
; TYPE: DNA
; ORGANISM: Human
US-09-900-448-1

Query Match 4.3%; Score 130; DB 11; Length 3186;

US-10-105-891-19
; Sequence 19, Application US/10105891
; Publication No. US20030073099A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhang, Jie
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NO. US20030073099A1el Nucleic Acids and
; FILE REFERENCE: 79ICIP2A
; CURRENT APPLICATION NUMBER: US/10/105,891
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/668,317
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/552,929
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: pt_FJ_genes Version 2.0
; SEQ ID NO 19
; LENGTH: 1631
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (71)..(1459)
US-10-105-891-19

Query Match 4.3%; Score 128.4; DB 10; Length 492;
Best Local Similarity 95.7%; Pred. No. 1e-26;
Matches 132; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2651 TGTGGTGTTCAGGGAGTTTGTGGAAGAGTCACAAATGGGACCGGAGTTAACT 2710
DB 255 TGCTGTGTTCAGGGAGTTTGTGGAAGAGTCACAAATGGGACCGGAGTTAACT 314
QY 2711 CAGAGATGGAAGATTTCACCCAGCCCTGTGGATGCTGCATTCGTCAGGTCAACA 2770
DB 315 CAGAGATGGAAGATTTCACCCAGCCCTGTGGATGCTGCATTCGTCAGGTCAACA 374
QY 2771 GTGCTTTCTGATCAAGG 2788
DB 375 GTGCTTTCTGATCAAGG 392

RESULT 11
US-09-960-352-3470
; Sequence 3470, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Mengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Machialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
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; SEQ ID NO 3470
; LENGTH: 225
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 15-LIB34-057-Q1-E1-D11
US-09-960-352-3470

Query Match      3.2%; Score 94.8; DB 9; Length 225;
Best Local Similarity 80.4%; Pred. No. 5.4e-17;
Matches 111; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2651 TGTGGGTTTTTTCAGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 2710
Db 38 TGTGTTTTTAAAGGGAGTTTGTGTGGAAGAGTCATGCTGGGCCCGGCAGTTGATCT 97

QY 2711 CAGAGAGATGGAAGAATTTCCCGAGCCCTGTGATGCTGCATTCCGTCAGGTCACAACA 2770
Db 98 CAGAGAGTGGGAAGAGTGGCCCGAGTCCCGTGGATGCTGCTGATTCCTGATGATCGTAACA 157

QY 2771 GTGTCCTTCTGATCAAGG 2788
Db 158 GTGTCCTTCTGATCAAGG 175

RESULT 12
US-09-960-352-7532
; Sequence 7532, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 7532
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 32-LIB34-054-Q1-E1-H7
US-09-960-352-7532

Query Match      3.2%; Score 94.8; DB 9; Length 237;
Best Local Similarity 80.4%; Pred. No. 5.4e-17;
Matches 111; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2651 TGTGGGTTTTTTCAGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 2710
Db 83 TGTGTTTTTAAAGGGAGTTTGTGTGGAAGAGTCATGCTGGGCCCGGCAGTTGATCT 142

QY 2711 CAGAGAGATGGAAGAATTTCCCGAGCCCTGTGATGCTGCATTCCGTCAGGTCACAACA 2770
Db 143 CAGAGAGTGGGAAGAGTGGCCCGAGTCCCGTGGATGCTGCATTCCGTCATGATCGTAACA 202

QY 2771 GTGTCCTTCTGATCAAGG 2788
Db 203 GTGTCCTTCTGATCAAGG 220

RESULT 13
US-09-960-352-2026
; Sequence 2026, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
```

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; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2026
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 09-LIB34-031-Q1-E1-C1
US-09-960-352-2026

Query Match      3.2%; Score 94.8; DB 9; Length 373;
Best Local Similarity 80.4%; Pred. No. 7.4e-17;
Matches 111; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2651 TGTGGGTTTTTTCAGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 2710
Db 106 TGTGTTTTTAAAGGGAGTTTGTGTGGAAGAGTCATGCTGGGCCCGGCAGTTGATCT 165

QY 2711 CAGAGAGATGGAAGAATTTCCCGAGCCCTGTGATGCTGCATTCCGTCAGGTCACAACA 2770
Db 166 CAGAGAGTGGGAAGAGTGGCCCGAGTCCCGTGGATGCTGCATTCCGTCATGATCGTAACA 225

QY 2771 GTGTCCTTCTGATCAAGG 2788
Db 226 GTGTCCTTCTGATCAAGG 243

RESULT 14
US-09-960-352-9132
; Sequence 9132, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9132
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 39-LIB34-014-Q1-E1-B4
US-09-960-352-9132

Query Match      3.2%; Score 94.8; DB 9; Length 384;
Best Local Similarity 80.4%; Pred. No. 7.6e-17;
Matches 111; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2651 TGTGGGTTTTTTCAGGGAGTTTGTGTGGAAGAGTCACAAATGGACCGGGAGTTAATCT 2710
Db 218 TGTGTTTTTAAAGGGAGTTTGTGTGGAAGAGTCATGCTGGGCCCGGCAGTTGATCT 277

QY 2711 CAGAGAGATGGAAGAATTTCCCGAGCCCTGTGATGCTGCATTCCGTCAGGTCACAACA 2770
Db 278 CAGAGAGTGGGAAGAGTGGCCCGAGTCCCGTGGATGCTGCATTCCGTCATGATCGTAACA 337

QY 2771 GTGTCCTTCTGATCAAGG 2788
Db 338 GTGTCCTTCTGATCAAGG 355

RESULT 15
US-09-960-352-4209
; Sequence 4209, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
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Search completed: June 8, 2004, 23:18:02
Job time : 830.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2004, 17:11:50 ; Search time 142 Seconds
(without alignments)
11724.315 Million cell updates/sec

Title: US-09-900-448-3_COPY_1_3000
Perfect score: 3000
Sequence: 1 tccctctccagccagccgcccc.....tggctgtttcagtcctag 3000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
C 1	60.8	2.0	7218	1	US-08-232-463-14
C 2	49.2	1.6	7218	1	US-08-232-463-14
C 3	43.6	1.5	92139	4	US-09-918-686-1
C 4	42.8	1.4	5852	1	US-07-867-106-2
C 5	42.6	1.4	38653	4	US-09-922-445-1
C 6	42	1.4	87350	3	US-08-781-891-79
C 7	42	1.4	87350	4	US-09-618-166-79
C 8	42	1.4	87543	4	US-09-791-211-3
C 9	41.2	1.4	505	4	US-09-621-976-15639
C 10	41	1.4	815	4	US-08-833-381-691
C 11	41	1.4	43795	3	US-08-742-185-101
C 12	41	1.4	118067	4	US-09-497-955A-32
C 13	40.8	1.4	569	4	US-08-461-325-44
C 14	40.8	1.4	569	4	US-10-012-542-44
C 15	40.8	1.4	1126	4	US-09-389-956-7
C 16	40.8	1.4	1210	4	US-09-443-041A-29
C 17	40.6	1.4	270	2	US-08-530-678A-30
C 18	40.6	1.4	270	3	US-08-897-126-30
C 19	40.6	1.4	969	4	US-09-023-655-66
C 20	40.4	1.3	832	4	US-09-621-976-2813
C 21	40.2	1.3	196	4	US-09-644-460-40
C 22	40.2	1.3	240	4	US-09-621-976-1324
C 23	40.2	1.3	249	4	US-09-621-976-1322
C 24	40.2	1.3	260	3	US-08-530-678A-29
C 25	40.2	1.3	260	2	US-08-897-126-29
C 26	40.2	1.3	675	4	US-08-621-976-2461
C 27	40.2	1.3	1560	4	US-09-227-357-34

Sequence 14, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 27, Appli
Sequence 3, Appli
Sequence 11, Appli
Sequence 1, Appli
Sequence 128, Appl
Sequence 4, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 1, Appli
Sequence 2813, Ap
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli

US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, P. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)833-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; LENGTH: 7218 base pairs
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PTZ9pt-Fis
US-08-232-463-14
Query Match 2.0%; Score 60.8; DB 1; Length 7218;

Matches 64; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 909 TCATTCACAAATATTTCTGGACAACTCTTATATGCGCAGGACACTTTTAGGAGTCAGG 968
DB 62345 TCAGTCAACAAATATTTATTTAGCACCTACTACTGTGCGCAGGCTCTGTTTGTAGTACTTGG 62286
QY 969 GATATATATGTTAAACAGACAGCGCAACAAAGCAA 1006
DB 62285 GGTACATCAGTGGACAAATTAACAGTAGAATATATAA 62248

RESULT 4

US-07-867-106-2
; Sequence 2, Application US/07867106
; Patent No. 5389526
; GENERAL INFORMATION:
; APPLICANT: Slade, Martin B
; APPLICANT: Chang, Andy C M
; APPLICANT: Williams, Keith L
; TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
; TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/867,106
; FILING DATE: 19926625
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PJ 7187
; APPLICATION NUMBER: PCT/AU90/00530
; FILING DATE: 02-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Feerey, Joanne Longo
; REGISTRATION NUMBER: 35,134
; REFERENCE/DOCKET NUMBER: RICE-0002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5852 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2378..5038
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2378..5038
US-07-867-106-2

Query Match 1.4%; Score 42.8; DB 1; Length 5852;
Best Local Similarity 50.0%; Pred. No. 0.089;
Matches 107; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 888 AATGATTTTTCATTTTTCATTCACAAATATTTCTGGACAACTCTTATATGCA 947
DB 5275 ATATTATCGTGCACTACTATTATTAATAAATACTTTAATAAATAATTTTAAACAT 5334
QY 948 GGCACATTTTTAGGAGTCGGGATATATATATGTTAAACAGACAGCGCAACAAAGCAA 1007

DB 5335 GGAAATTTATATAGATCGATAGATCACTAATTTTAAATTAATATATTTATAA 5394
QY 1008 GCAACAAACACATCACAGATAAGTAGACAGATGAAGAATTTTCAAGTTTATAGTA 1067
DB 5395 AAATTTGAAGTTTCATCAAGATATATAGATAATTTTATTTTGAATTTTAAAAA 5454
QY 1068 AAATAAACAAGCAAGGCTCTGAAATGCTAGAT 1101
DB 5455 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5488

RESULT 5
US-09-922-445-1/c
; Sequence 1, Application US/09922445
; Patent No. 6528268
; GENERAL INFORMATION:
; APPLICANT: Andersson, Maria K.
; APPLICANT: Berglund, Lars G. T.
; APPLICANT: Reneland, Rikard H.
; APPLICANT: Adam, Gail I. R.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
; FILE REFERENCE: CG126US
; CURRENT APPLICATION NUMBER: US/09/922,445
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 38653
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: 5' UTR
; LOCATION: (1)..(26156)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (24801)..(24801)
; OTHER INFORMATION: nucleotide 24801 is a single nucleotide polymorphism which can be
; OTHER INFORMATION: A or G
; NAME/KEY: misc feature
; LOCATION: (24941)..(24941)
; OTHER INFORMATION: nucleotide 24941 is a single nucleotide polymorphism which can be
; OTHER INFORMATION: T or C
; NAME/KEY: exon
; LOCATION: (26157)..(26252)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (26253)..(26401)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (26402)..(26543)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (26544)..(27024)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (27025)..(27178)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (27179)..(30519)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (27645)..(27645)
; OTHER INFORMATION: nucleotide 27645 is a single nucleotide polymorphism which can be
; OTHER INFORMATION: C or G
; NAME/KEY: exon
; LOCATION: (30520)..(30681)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (30682)..(30894)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (30895)..(31027)

OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (31028)..(31747)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (31748)..(31841)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (31842)..(32400)
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: (32163)..(32163)
OTHER INFORMATION: nucleotide 32163 is a single nucleotide polymorphism which can be
OTHER INFORMATION: A or C
NAME/KEY: exon
LOCATION: (32401)..(32528)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (32529)..(33414)
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: (32614)..(32614)
OTHER INFORMATION: nucleotide 32614 is a single nucleotide polymorphism which can be
OTHER INFORMATION: A or G
NAME/KEY: exon
LOCATION: (33415)..(33597)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (33598)..(34314)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (34315)..(34588)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (34589)..(36404)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (36405)..(36523)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (36524)..(38341)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (38342)..(38653)
OTHER INFORMATION:
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank/AC004923
DATABASE ENTRY DATE: 1999-12-21
RELEVANT RESIDUES: (1)..(38653)
US-09-922-445-1

Query Match 1.4%; Score 42.6; DB 4; Length 38653;
Best Local Similarity 67.4%; Pred. No. 0.4;
Matches 60; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 904 TTTTTCATTCACAAATATTTCTGGAACAACCTCTTATATGCCAGGCACTATTTTAGGAG 963
Db 14573 TGTATATGCGCAACTATTTGCTGAGCACTACTATGTCACAGGTACTGTTCTAGGCT 14514
QY 964 TCAGGGATATATATGTTAAACAACAGACAG 992
Db 14513 CTGGGGATATAGCAGAGATAAACACAG 14485

RESULT 6
US-08-781-891-79
Sequence 79, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.

APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-79

Query Match 1.4%; Score 42; DB 3; Length 87350;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 60; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 911 ATTCAACAATATTTCTGGAACAACCTCTTATATGCCAGGCACTATTTTAGGAGTCAGGGA 970
Db 64933 ATTCAACAATATTTATTTAGCACTTACTATGTCGAGGCACTGTTGTGTAGTCTGG 64992
QY 971 TATATATGTTAAACAACAGACAGCAAAACA 1000
Db 64993 ATTACCAATGACAAACAAAAGTGAACA 65022

RESULT 7
US-09-618-166-79
Sequence 79, Application US/09618166
Patent No. 6583112
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
Yu, Chang-En
Oshima, Junko
Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
WERNER'S SYNDROME

NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/618,166
;; FILING DATE: 17-Jul-2000
;; CLASSIFICATION: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McMasters, David D.
;; REGISTRATION NUMBER: 33,963
;; REFERENCE/DOCKET NUMBER: 240052.419C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 79:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 87350 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-618-166-79
Query Match 1.48; Score 42; DB 4; Length 87350;
Best Local Similarity 66.7%; Pred. No. 1.1; Mismatches 0; Gaps 0;
Matches 60; Conservative 0; Indels 30; Gaps 0;
Qy 911 ATTCAACAAATATTCTGGACAACTCTTATATGCCAGGCACTATTTAGAGTCAGGGA 970
Db 64933 ATTCAACAAATATTATGACCACTTACTATGTGCCAGGCACTGTGTGTAGGTGCTGG 64992
Qy 971 TATATATGTTAAACACAGCAGGCAAAACA 1000
Db 64993 AATACAGCAATGAACAAAAAAGTGAACA 65022
RESULT 8
US-09-791-211-3
Sequence 3, Application US/09791211
Patent No. 6448080
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RIS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 3
LENGTH: 87543
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: 7421
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 7427
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 11609
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 12605
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NAME/KEY: unsure
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LOCATION: 54684
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OTHER INFORMATION: unknown

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; NAME/KEY: unsure
; LOCATION: 59235
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59242
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 63290
; OTHER INFORMATION: unknown
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; OTHER INFORMATION:
; US-09-791-211-3

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Best Local Similarity 1.4%; Score 42; DB 4; Length 87543;
Matches 60; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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QY 971 TATATATGGTAACAGACAGGCAAAACA 1000
DB 65186 AATACAGCAATGAACAAAAAAGTGAACA 65215

RESULT 9
US-09-621-976-15639/c
; Sequence 15639, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S. J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15639
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens

; NAME/KEY: unsure
; LOCATION: 59235
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 59242
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; OTHER INFORMATION:
; US-09-791-211-3

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Best Local Similarity 1.4%; Score 41.2; DB 4; Length 505;
Matches 49; Conservative 146; Mismatches 119; Indels 4; Gaps 2;

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QY 411 TTCOGAATGTGTGTTTCTGTTGGAAGGAACTTCCGACAGTAGTAAAGGATCTGAG 470
DB 308 WSKKXTRWCTCTSWRKYMWMSCGWARSMKSWARSYSNMACWMMMSASAYFARRSMYGAR 249
QY 471 ACTTTTGTAAATATATATGAGGACTGTGAGGGGTCTGAGGCCATCTGTGAGGATCAG 530
DB 248 RSMRAGAGNWRARRKGRKRSKMSKMSKMSKMSKMSKMSKMSKMSKMSKMSKMSKMSKMS 189
QY 531 GGCCCTTTGAGCCTTGGCTAGGAGAGGGGCTCTGGAACTTCATCTGCCGCCATAGCTG 590
DB 188 SKCMS---CRGTCAKWRVYARYAKRYASSMGKYMNGCRWCYAKKARMYGYVASRSRSTGS 132
QY 591 AGTCGCCCCATAATCTCTTTCTGACTCTAGGCAATCTCACACAGAAATGGGCAGCT 650
DB 131 RCKYRRRRRMYMWMYKYMWMYKYMWMYKYMWMYKYMWMYKYMWMYKYMWMYKYMWMYK 72
QY 651 TTGGAGTGGGCCAGGA 668
DB 71 MMRCWRSRYRCWMSGKW 54

RESULT 10
US-09-833-381-691
; Sequence 691, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833.381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516.448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 691
; LENGTH: 815
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(815)
; OTHER INFORMATION: n = A,T,C or G
; US-09-833-381-691

Query Match
Best Local Similarity 1.4%; Score 41; DB 4; Length 815;
Matches 59; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 2301 CTGACTCCCTAAGTCTGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2360
DB 40 CTACCTCAAGAGTAGCTTCCCGAATGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 99
QY 2361 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2389
DB 100 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 128

RESULT 11
US-08-742-185-101
; Sequence 101, Application US/08742185
; Patent No. 6020476
; GENERAL INFORMATION:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
OM nucleic - nucleic search, using sw model
Run on: June 8, 2004, 18:54:10 ; Search time 829.5 Seconds
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16499.081 Million cell updates/sec

Title: US-09-900-448-3_COPY_3001_6000
Perfect score: 3000
Sequence: 1 tcttagttctacacgcgtct.....ctccattgtatcaactgtgt 3000

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2995936 seqs, 228098010 residues

Total number of hits satisfying chosen parameters: 5391872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
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14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3000	100.0	13737	11	US-09-900-448-3
2	457.6	15.3	533	10	US-09-918-995-31396
3	445.2	14.8	495	10	US-09-918-995-32463
4	441.6	14.7	480	10	US-09-918-995-31405
5	441.4	14.7	494	10	US-09-918-995-31407
6	440.8	14.7	478	10	US-09-918-995-31269
7	217.6	7.3	1631	15	US-10-125-237-19
8	217.6	7.3	1631	15	US-10-105-891-19
9	167.4	5.6	473	10	US-09-918-995-32181
10	161.4	5.4	3186	11	US-09-900-448-1
11	159.6	5.3	1516	15	US-10-175-523-84
12	159.6	5.3	1516	15	US-10-316-253-39
13	157.8	5.3	367	9	US-09-960-352-2954
14	157.8	5.3	422	9	US-09-960-352-14163

Sequence 421, App	15	154.6	5.2	393	9	US-09-960-352-421
Sequence 8960, App	16	151.4	5.0	415	9	US-09-960-352-8960
Sequence 8005, App	17	142.4	4.7	385	9	US-09-960-352-8005
Sequence 10754, A	18	135	4.5	488	10	US-09-918-995-30754
Sequence 32820, A	19	133.4	4.4	491	10	US-09-918-995-32820
Sequence 1099, App	20	126.4	4.2	261	11	US-09-864-408A-1099
Sequence 12958, A	21	121	4.0	315	9	US-09-960-352-12958
Sequence 5375, App	22	110.8	3.7	374	9	US-09-960-352-5375
Sequence 898, App	23	109.2	3.6	396	9	US-09-960-352-8898
Sequence 380, App	24	108.8	3.6	437	9	US-09-960-352-380
Sequence 6078, App	25	104.4	3.5	379	9	US-09-960-352-6078
Sequence 4685, App	26	99.6	3.3	271	9	US-09-960-352-4685
Sequence 445, App	27	93.2	3.1	405	9	US-09-960-352-445
Sequence 2026, App	28	90	3.0	373	9	US-09-960-352-2026
Sequence 30828, A	29	86	2.9	488	10	US-09-918-995-30828
Sequence 31395, A	30	79.2	2.6	422	10	US-09-918-995-31395
Sequence 8595, App	31	77	2.6	422	10	US-09-918-995-8595
Sequence 3702, App	32	65.4	2.2	425	9	US-09-960-352-3702
Sequence 431, App	33	64.8	2.2	225	9	US-09-960-352-431
Sequence 5368, App	34	62.8	2.1	374	9	US-09-960-352-5368
Sequence 12936, A	35	62.8	2.1	397	9	US-09-960-352-12936
Sequence 6846, App	36	61.2	2.0	383	9	US-09-960-352-6846
Sequence 10449, A	37	60	2.0	60	10	US-09-908-975-10449
Sequence 12972, A	38	59.6	2.0	343	9	US-09-960-352-12972
Sequence 182, App	39	58.4	1.9	1128	10	US-09-933-767-182
Sequence 182, App	40	58.4	1.9	1128	13	US-10-004-860-182
Sequence 182, App	41	58.4	1.9	1128	15	US-10-023-282-182
Sequence 24, Appl	42	58.4	1.9	2630	9	US-09-880-192-24
Sequence 31, Appl	43	58.4	1.9	2630	15	US-10-427-348-24
Sequence 31, Appl	44	58.4	1.9	4360	15	US-10-287-218-31
Sequence 1159, App	45	55.2	1.8	7524	9	US-09-764-847-1159

ALIGNMENTS

RESULT 1

US-09-900-448-3
; Sequence 3, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
; APPLICANT: CECARDI, Toni et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001272
; CURRENT APPLICATION NUMBER: US/09/900,448
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: Human
US-09-900-448-3

Query Match	100.0%;	Score	3000;	DB	11;	Length	13737;
Best local similarity	100.0%;	Pred. No.	0;				
Matches	3000;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	3001	TCTTAGTTCCTACACCGCTCTGCTGTACTC	CACACTGCTGCCCATCTCTTTTCTCTGGC	3060			
Qy	61	AATTGCTTCCTGCTTCCATCACTGATCAAGTCTCTTTCATAGGGCAAGGAACT	120				
Db	3061	AATTGCTTCCTGCTTCCATCACTGATCAAGTCTCTTTCATAGGGCAAGGAACT	3120				
Qy	121	TGTTCCCAACAACTGCGCTAGAGAGCATGTGAGCATGAAATCCAGTCTGCT	180				
Db	3121	TGTTCCCAACAACTGCGCTAGAGAGCATGTGAGCATGAAATCCAGTCTGCT	3180				
Qy	181	GTGCTCACCAGTCCCATGTGACCCAGGCTGTCTGCTCAGAGGAGGGGTGCTTTC	240				

QY	2401	TACTACTGCTTCCAGGGTAACCAATTCCTGGCGTTTCGACCCCTCTCAGGGGAGAGGTGCCT	2460
Db	5401	TACTACTGCTTCCAGGGTAACCAATTCCTGGCGTTTCGACCCCTCTCAGGGGAGAGGTGCCT	5460
QY	2461	CCCAGGTACCGCGGGATGTCCGAGACTACTTCATGCGCTGCCCTGCCAGAGGTGAGAAA	2520
Db	5461	CCCAGGTACCGCGGGATGTCCGAGACTACTTCATGCGCTGCCCTGCCAGAGGTGAGAAA	5520
QY	2521	GCCTTAGCACTTCAGACCTGTGAGAAATTCATCCACTTTCCTCTGAGCTGTGGATCTCAAG	2580
Db	5521	GCCTTAGCACTTCAGACCTGTGAGAAATTCATCCACTTTCCTCTGAGCTGTGGATCTCAAG	5580
QY	2581	TGTCCTAGCTCTCACTTTAACTCCGTGTGGGACACCTTGGGCCCTTAAATCTAGCCCAATT	2640
Db	5581	TGTCCTAGCTCTCACTTTAACTCCGTGTGGGACACCTTGGGCCCTTAAATCTAGCCCAATT	5640
QY	2641	TCCATTCTGATTTTCCCATTTGCCCTCATATGCGGAAACCCACACCCCACTTAACCCCGCAG	2700
Db	5641	TCCATTCTGATTTTCCCATTTGCCCTCATATGCGGAAACCCACACCCCACTTAACCCCGCAG	5700
QY	2701	CACTCTCTCCACCTTGGACCTCACTCTGACCTCTGGCCCTCTCTCTGTCTCTCTCAACC	2760
Db	5701	CACTCTCTCCACCTTGGACCTCACTCTGACCTCTGGCCCTCTCTCTGTCTCTCTCAACC	5760
QY	2761	ATTCTCTCTCCAGGCCATGGACACAGGAATGGGACTGGCCATGGGACAGTACCCACCA	2820
Db	5761	ATTCTCTCTCCAGGCCATGGACACAGGAATGGGACTGGCCATGGGACAGTACCCACCA	5820
QY	2821	TGGCCCTCGATATATGCGCTGTAGCCACACACTAGTCTGTCTGCACTGACGTCTGACAA	2880
Db	5821	TGGCCCTCGATATATGCGCTGTAGCCACACACTAGTCTGTCTGCACTGACGTCTGACAA	5880
QY	2881	CCATGTGCGACCTATGCTCTCAGTGTGAGAGATGCCCCCACTCCCCCAATGTGCTCT	2940
Db	5881	CCATGTGCGACCTATGCTCTCAGTGTGAGAGATGCCCCCACTCCCCCAATGTGCTCT	5940
QY	2941	CACATCTCTTTTACTGTATCTCCCATCTTGACACATTTCTCAATGTGTCATCACTGTGT	3000
Db	5941	CACATCTCTTTTACTGTATCTCCCATCTTGACACATTTCTCAATGTGTCATCACTGTGT	6000
RESULT 2			
US-09-918-995-31396			
; Sequence 31396, Application US/0918995			
; Publication No. US20030073623A1			
; GENERAL INFORMATION:			
; APPLICANT: Hyseq, Inc.			
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED			
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES			
; FILE REFERENCE: 20411-756			
; CURRENT APPLICATION NUMBER: US/09/918,995			
; CURRENT FILING DATE: 2001-07-30			
; PRIOR FILING DATE: 1999-01-20			
; NUMBER OF SEQ ID NOS: 38054			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 31396			
; LENGTH: 533			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (1)...(533)			
; OTHER INFORMATION: n = A,T,C or G			
US-09-918-995-31396			
Query March 15.3%; Score 457.6; DB 10; Length 533;			
Best Local Similarity 98.9%; Pred. No. 1.4e-131;			
Matches 460; Conservative 0; Mismatches 5; Indels 0; Gaps 0;			
QY	1479	GAGAAAGATACCCAAAGTCTCTCCAGATGAAATTCCTGGAAATCCCATCCCACTGGAT	1538

D	b	68	GAGAAAGGATACCCAAAGTTGTCTCCAAGATGAATTTTCTCGAATCCATCCCCCACTGGAT	127
Q	y	1539	GCAGCTGTGGAAATGTTCACCGTGAGAAATGTCAAAGTGAAGCGGTCTCTTTCTTCCAAAGT	1598
D	b	128	GCAGCTGTGGAAATGTTCACCGTGAGAAATGTCAAAGTGAAGCGGTCTCTTTCTTCCAAAGT	187
Q	y	1599	CAGTCCAGGCTGGAAATCACAAGAACCTGGAGTAGTGTGGTGTGATGATGCCAGTAGT	1658
D	b	188	CAGTCCAGGCTGGAAATCACAAGAACCTGGAGTAGTGTGGTGTGATGATGCCAGTAGT	247
Q	y	1659	GATGGTGATAGTGGTATCATGTGTGGTGGAGGACCATTATGTGGCTTTTTTAAGAAGGG	1718
D	b	248	GATGGTGATAGTGGTATCATGTGTGGTGGAGCCACTATGTGGCTTTTTTAAGAAGGG	307
Q	y	1719	AATATAGAAAGCCACGTATGGCTATAGAGTCACTGTAGGGAGAGAGAGAGTCAATCTG	1778
D	b	308	AATATAGAAAGCCACGTATGGCTATAGAGTCACTGTAGGGAGAGAGAGTCAATCTG	367
Q	y	1779	GTGAAGGCAACTGTGTGTAATCTGTGTGAATAGTCCCTCATTTGTCGCCCAATGCCCTTA	1818
D	b	368	GTGAAGGCAACTGTGTGTAATCTGTGTGAATAGTCCCTCATTTGTCGCCCAATGCCCTTA	427
Q	y	1839	GGACAAATCTACCCCTCTTTAGTCTTACATACAAAGTCTCTCCATGGCCAAATGCCCTATGG	1898
D	b	428	NGACAAATCTACCCCTCTTTAGTCTTACATACAAAGTCTCTCCATGGCCAAATGCCCTATGG	487
Q	y	1899	CCCTTCAGCTTTCAGCTTTTATTTATATCTTTTACCTTTAACACATAAGC	1943
D	b	488	CCCTTCAGCTTTCAGCTTTTATTTATATCTTTTACCTTTAACACATAAGC	532
 RESULT 3:				
US-09-918-995-32463				
; Sequence 32463, Application US/09918995				
; Publication No. US20030073623A1				
; GENERAL INFORMATION:				
; APPLICANT: Hyseq, Inc.				
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED				
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES				
; FILE REFERENCE: 20411-756				
; CURRENT APPLICATION NUMBER: US/09/918,995				
; CURRENT FILING DATE: 2001-07-30				
; PRIOR APPLICATION NUMBER: US/09/235,076				
; PRIOR FILING DATE: 1999-01-20				
; NUMBER OF SEQ ID NOS: 38054				
; SOFTWARE: FastSeq for Windows Version 3.0				
; SEQ ID NO 32463				
; LENGTH: 495				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
; FEATURE:				
; NAME/KEY: misc_feature				
; LOCATION: (1)..(495)				
; OTHER INFORMATION: n = A,T,C or G				
US-09-918-995-32463				
 Query Match 14.8%; Score 445.2; DB 10; Length 495;				
Best Local Similarity 99.3%; Pred.No. 9.8e-128;				
Matches 447; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
Q	y	1908	TTTCAGCTTTTATATATCTTTTACCTTAACACTAAGCTCCAGAAACCCATGCTATTCTCT	1967
D	b	46	TCCTGACCTTTTATATATCTTTTACCTTAACACTAAGCTCCAGAAACCCATGCTATTCTCT	105
Q	y	1968	GTACACTCAGTTGCTCCAGTCTTTGGAATCTTCTCTCTCTGGGGTTCATCTCTCT	2027
D	b	106	GTACACTCAGTTGCTCCAGTCTTTGGAATCTTCTCTCTCTGGGGTTCATCTCTCT	165
Q	y	2028	TGTCGCTCTTTTAAATCTCTACTTCAGATTTTACCTTTAAGTATCATCTTCCCTGGGAAGTT	2087
D	b	166	TGTCGCTCTTTTAAATCTCTACTTCAGATTTTACCTTTAAGTATCATCTTCCCTGGGAAGTT	225
Q	y	2088	TTCCCAGACTCTCCCCACTGCCTTTGCTGAGCTGATCCTGTGTGTTTGTGCTGAATTT	2147

Db 226 TTCCGAGCTCTCCACATGCTTCTGAGCTGATCTCTGCTGCTGAATTT 285
Qy 2148 TGTGTATGATACACCTCTCTTTAGCCATCTCTCTGATGGCTGTGAGCTCATGTGTGAG 2207
Db 286 TGTGTATGATACACCTCTCTTTAGCCATCTCTCTGATGGCTGTGAGCTCATGTGTGAG 345
Qy 2208 TACCATTTATCTGGCCATCTCTGGACCCAGAGAAAGCACAAGGAGGGGTAAACCCGGTC 2267
Db 346 TACATTATCTGGCCATCTCTGGACCCAGAGAAAGCACAAGGAGGGGTAAACCCGGTC 405
Qy 2268 TCACCAAAATGCTGTGATGATTTGACAAAGGTGACCCGAGTGGTTCTGGGACTTGGC 2327
Db 406 TCACCAAAATGCTGTGATGATTTGACAAAGGTGACCCGAGTGGTTCTGGGACTTGGC 465
Qy 2328 TAGCGGAAACCATGAGGAGGCTTCTGGCC 2357
Db 466 TAGCGGAAACCATGAGGAGGCTTCTGGCC 495

RESULT 4
US-09-918-995-31405
; Sequence 31405, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31405
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(480)
; OTHER INFORMATION: n = A, T, C or G
US-09-918-995-31405

Query Match 14.7%; Score 441.6; DB 10; Length 480;
Best Local Similarity 99.1%; Pred. No. 1.3e-126;
Matches 444; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1908 TTTCAGCTTTTATATATACCTTTACCTTAACACTAGCTCCAGAAACCTATGCTATTCTCT 1967
Db 32 TCTGACTTTTATATATATCTTTTACCTTAACACTAGCTCCAGAAACCTATGCTATTCTCT 91
Qy 1968 GTACACTCAGTTTGTCTCCATGCTTTGGAATCTTCTCTCTCTCTGGGTTCCACTCTCT 2027
Db 92 GTACACTCAGTTTGTCTCCATGCTTTGGAATCTTCTCTCTCTCTGGGTTCCACTCTCTCT 151
Qy 2028 TGTGTGCTTTTAAATCTCTACTTCAGATTCACTTTAAGTATCATCTTCCCTGGGAGTT 2087
Db 152 TGTGTGCTTTTAAATCTCTACTTCAGATTCACTTTAAGTATCATCTTCCCTGGGAGTT 211
Qy 2088 TTCCAGACTCTCCCACTGCTTTGCTGAGCTGATCTGTGTGCTTTTGTGCTGAATTT 2147
Db 212 TTCCAGACTCTCCCACTGCTTTGCTGAGCTGATCTGTGTGCTTTTGTGCTGAATTT 271
Qy 2148 TGTGTATGATACACCTCTCTTTAGCCATCTCTCTGATGGCTGTGAGCTCCATGTGTGAG 2207
Db 272 TGTGTATGATACACCTCTCTTTAGCCATCTCTCTGATGGCTGTGAGCTCCATGTGTGAG 331
Qy 2208 TACCATTTATCTGGCCATCTCTGGACCCAGAGAAAGCACAAGGAGGGGTAAACCCGGTC 2267
Db 332 TACCATTTATCTGGCCATCTCTGGACCCAGAGAAAGCACAAGGAGGGGTAAACCCGGTC 391

Qy 2268 TCACCAAAATGCTGTGATGATTTGACAAAGGTGACCCGAGTGGTTCTGGGACTTGGC 2327
Db 392 TCACCAAAATGCTGTGATGATTTGACAAAGGTGACCCGAGTGGTTCTGGGACTTGGC 451
Qy 2328 TAGCGGAAACCATGAGGAGGCTTCTGG 2355
Db 452 TAGCGGAAACCATGAGGAGGCTTCTGG 479

RESULT 5
US-09-918-995-31407
; Sequence 31407, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31407
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(494)
; OTHER INFORMATION: n = A, T, C or G
US-09-918-995-31407

Query Match 14.7%; Score 441.4; DB 10; Length 494;
Best Local Similarity 99.8%; Pred. No. 1.5e-126;
Matches 442; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1908 TTTCAGCTTTTATATATACCTTTTACCTTAACACTAGCTCCAGAAACCTATGCTATTCTCT 1967
Db 52 TCTGACTTTTATATATATCTTTTACCTTAACACTAGCTCCAGAAACCTATGCTATTCTCT 111
Qy 1968 GTACACTCAGTTTGTCTCCATGCTTTGGAATCTTCTCTCTCTGGGTTCCACTCTCTCT 2027
Db 112 GTACACTCAGTTTGTCTCCATGCTTTGGAATCTTCTCTCTCTGGGTTCCACTCTCTCTCT 171
Qy 2028 TGTGTGCTTTTAAATCTCTACTTCAGATTCACTTTAAGTATCATCTTCCCTGGGAGTT 2087
Db 172 TGTGTGCTTTTAAATCTCTACTTCAGATTCACTTTAAGTATCATCTTCCCTGGGAGTT 231
Qy 2088 TTCCAGACTCTCCCACTGCTTTTGTGAGCTGATCTGTGTGCTTTTGTGCTGAATTT 2147
Db 232 TTCCAGACTCTCCCACTGCTTTTGTGAGCTGATCTGTGTGCTTTTGTGCTGAATTT 291
Qy 2148 TGTGTATGATACACCTCTCTTTAGCCATCTCTCTGATGGCTGTGAGCTCCATGTGTGAG 2207
Db 292 TGTGTATGATACACCTCTCTTTAGCCATCTCTCTGATGGCTGTGAGCTCCATGTGTGAG 351
Qy 2208 TACCATTTATCTGGCCATCTCTGGACCCAGAGAAAGCACAAGGAGGGGTAAACCCGGTC 2267
Db 352 TACCATTTATCTGGCCATCTCTGGACCCAGAGAAAGCACAAGGAGGGGTAAACCCGGTC 411
Qy 2268 TCACCAAAATGCTGTGATGATTTGACAAAGGTGACCCGAGTGGTTCTGGGACTTGGC 2327
Db 412 TCACCAAAATGCTGTGATGATTTGACAAAGGTGACCCGAGTGGTTCTGGGACTTGGC 471
Qy 2328 TAGCGGAAACCATGAGGAGGCTT 2350
Db 472 TAGCGGAAACCATGAGGAGGCTT 494

RESULT 6
US-09-918-995-31269

Sequence 31269, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31269
LENGTH: 478
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(478)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31269

Query Match 14.7%; Score 440.8; DB 10; Length 478;
Best Local Similarity 99.5%; Pred. No. 2.3e-126;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1908 TTGACTGTTTATATATACCTTAACACTAAGCTCCAGAAACCTATGCTATCTCT 1967
DB 34 CTGACTTTTATATATATACCTTAACACTAAGCTCCAGAAACCTATGCTATCTCT 93
QY 1968 GTACACTGAGTTTGTCTCCATGCTTTTGGAAATCTTCTCTCTGCGGTTCCATCTCTCT 2027
DB 94 GTACACTGAGTTTGTCTCCATGCTTTTGGAAATCTTCTCTCTGCGGTTCCATCTCTCT 153
QY 2028 TGTGTGCTTTTAACTTCTTCACTTCACTTTAAGTATCATCTTCCCTGGAGTT 2087
DB 154 TGTGTGCTTTTAACTTCTTCACTTCACTTTAAGTATCATCTTCCCTGGAGTT 213
QY 2088 TTCCAGAGCTCTCCCACTGCTTCTGAGCTGATCTCTGTTGTTTGTCTGCTGAATTT 2147
DB 214 TTCCAGAGCTCTCCCACTGCTTCTGAGCTGATCTCTGTTGTTTGTCTGCTGAATTT 273
QY 2148 TGTGTATGATCACTCTCTTTAGCCATCTCTGATGCTGTGAGCTCCATGCTGCTAG 2207
DB 274 TGTGTATGATCACTCTCTTTAGCCATCTCTGATGCTGTGAGCTCCATGCTGCTAG 333
QY 2208 TACCATTTCTGCCCCATCTCTGAGCCACAGAAAGCGGGGTAAACCGGTC 2267
DB 334 TACCATTTCTGCCCCATCTCTGAGCCACAGAAAGCGGGGTAAACCGGTC 393
QY 2268 TCACCAATGCTCTGTTGATTGATTGACAAAGTGACCGAGTGCTTCTGGAGTTGCT 2327
DB 394 TCACCAATGCTCTGTTGATTGATTGACAAAGTGACCGAGTGCTTCTGAGCTTGGC 453
QY 2328 TACGGGAACATGACGAGGCTC 2351
DB 454 TACGGGAACATGACGAGGCTC 477

RESULT 7
US-10-125-237-19
Sequence 19, Application US/10125237
Publication No. US2003002239A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Felyan
APPLICANT: Zhao, Qing A.
APPLICANT: Xue, Aidong J.
APPLICANT: Zhang, Jie

APPLICANT: Wehrman, Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US2003002239A1el Nucleic Acids and
Polypeptides
FILE REFERENCE: 79ICIP2AIV
CURRENT APPLICATION NUMBER: US/10/125,237
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 09/668,317
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 91
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 19
LENGTH: 1631
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (71)..(1459)
US-10-125-237-19
Query Match 7.3%; Score 217.6; DB 15; Length 1631;
Best Local Similarity 98.2%; Pred. No. 3.4e-56;
Matches 220; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2290 TTGGACAAAGGTGACCGGAGTGGTTCTGGGACTTGGCTACGGGAACCATGAAGGAGCT 2349
DB 551 TTCCTCCAGGTGACCGGAGTGGTTCTGGGACTTGGCTACGGGAACCATGAAGGAGCT 610
QY 2350 TCTGCGCAGCTTTTGGAACTGCTCTGCTGCTGAGATGCTGCGCGCTACTACTGCT 2409
DB 611 TCTGCGCAGCTTTTGGAACTGCTCTGCTGCTGAGATGCTGCGCGCTACTACTGCT 670
QY 2410 TTCCAGGGTAACTTCTGCTGCTTCCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2469
DB 671 TTCCAGGGTAACTTCTGCTGCTTCCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 730
QY 2470 CCGCGGGATGTCGAGACTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2513
DB 731 CCGCGGGATGTCGAGACTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 774

RESULT 8
US-10-105-891-19
Sequence 19, Application US/10105891
Publication No. US20030073099A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Felyan
APPLICANT: Zhao, Qing A.
APPLICANT: Xue, Aidong J.
APPLICANT: Zhang, Jie
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030073099A1el Nucleic Acids and
Polypeptides
FILE REFERENCE: 79ICIP2A
CURRENT APPLICATION NUMBER: US/10/105,891
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: 09/668,317
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 91
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 19
LENGTH: 1631

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (71)..(1459)
US-10-105-891-19

Query Match
Best Local Similarity 7.3%; Score 217.6; DB 15; Length 1631;
Matches 220; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2290 TTGACAAAGGTGACCGCGAGTGGTCTGGGACTTGGCTACGGGAACCAATGAGGAGCGT 2349
Db 551 TTCTTCCAGGTGACCGCGAGTGGTCTGGGACTTGGCTACGGGAACCAATGAGGAGCGT 610
QY 2350 TCTGGCCAGCTGTGGGAACTGCTCTCTGCTGCTGAGATGGCTGGCCGCTACTACTGC 2409
Db 611 TCTGGCCAGCTGTGGGAACTGCTCTCTGCTGCTGAGATGGCTGGCCGCTACTACTGC 670
QY 2410 TTCCAGGGTAACCAATTCCTGGCTTCGACCTCTGACGGGAGAGTGCTCCCGAGGTAC 2469
Db 671 TTCCAGGGTAACCAATTCCTGGCTTCGACCTCTGACGGGAGAGTGCTCCCGAGGTAC 730
QY 2470 CCGCGGAGTCCGAGACTTTCATGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2513
Db 731 CCGCGGAGTCCGAGACTTTCATGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 774

RESULT 9
US-09-918-995-32181
; Sequence 32181, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 32181
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(473)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32181

Query Match
Best Local Similarity 5.6%; Score 167.4; DB 10; Length 473;
Matches 174; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2327 CTACGGGAACCATGAGAGCGTTCCTGGCCAGCTGTGGGAATGCTCTGCTGCTGCA 2386
Db 12 CTACGCTAGNACGCGCAATTCCTGCGCCAGCTGTGGGAATGCTCTGCTGCTGCA 71
QY 2387 GATGCTGGCGCGCTACTACTGCTTCCAGGTAACCAATTCCTGCGCTTGGACCTGCA 2446
Db 72 GATGCTGGCGCGCTACTACTGCTTCCAGGTAACCAATTCCTGCGCTTGGACCTGCA 131
QY 2447 GGGGAGAGGTGCTCCCGAGGTACCGGGAGTGCAGAGACTTATGCGCCGCTG 2506
Db 132 GGGGAGAGGTGCTCCCGAGGTACCGGGAGTGCAGAGACTTATGCGCCGCTG 191
QY 2507 GCAGAGG 2513
Db 192 GCAGAGG 198
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```

RESULT 10
US-09-900-448-1
; Sequence 1, Application US/09900448
; Publication No. US20030220488A1
; GENERAL INFORMATION:
; APPLICANT: CECCARDI, Toni et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: CL001272
; CURRENT APPLICATION NUMBER: US/09/900,448
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3186
; TYPE: DNA
; ORGANISM: Human
US-09-900-448-1

Query Match
Best Local Similarity 5.4%; Score 161.4; DB 11; Length 3186;
Matches 165; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1430 CTTTGTGATGCGAGGGGACAAAGTCTGGGTATACCTCTCTGAAAGCAAGGAAAGGATA 1489
Db 338 CTTTGTGATGCGAGGGGACAAAGTCTGGGTATACCTCTCTGAAAGCAAGGAAAGGATA 397
QY 1490 CCAAGAGTTGCTCCAAGATGATTTCTTGGAAATCCCATCCCACTGGATCGAGCTGTGGA 1549
Db 398 CCAAGAGTTGCTCCAAGATGATTTCTTGGAAATCCCATCCCACTGGATCGAGCTGTGGA 457
QY 1550 ATGTCACTGCGAGGATGCAAGCTGCAAGCGTCTCTTCTTCCAGGTCGA 1600
Db 458 ATGTCACTGCGAGGATGCAAGCTGCAAGCGTCTCTTCTTCCAGGTCGA 508

RESULT 11
US-10-175-523-84
; Sequence 84, Application US/10175523
; Publication No. US20030096264A1
; GENERAL INFORMATION:
; APPLICANT: Brockman, Jeffrey
; APPLICANT: Evans, David
; APPLICANT: Hook, Derek
; APPLICANT: Klimczak, Leszek
; APPLICANT: Laeferg, Pascal
; APPLICANT: Palfreyman, Michael
; APPLICANT: Rajan, Priithi
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
; FILE REFERENCE: 3235/1J795-US3
; CURRENT APPLICATION NUMBER: US/10/175,523
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,151
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 84
; LENGTH: 1516
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-175-523-84
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Search completed: June 8, 2004, 23:18:04
Job time : 831.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 8, 2004, 17:11:50 ; Search time 142 Seconds
(without alignments)
11724.315 Million cell updates/sec

Title: US-09-900-448-3_COPY_3001_6000

Perfect score: 3000

Sequence: 1 tcttagttctacacgctct.....ctccattgtcatcactgtgt 3000

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA.*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81.8	2.7	7218	1	US-08-232-463-14
2	70.8	2.4	7218	1	US-08-232-463-14
3	58.4	1.9	1128	4	US-09-205-258-182
4	48.8	1.6	619	4	US-09-489-847-58
5	48	1.6	22376	4	US-09-269-939A-19
6	47.6	1.6	44453	4	US-09-146-053-5
7	47	1.6	28720	4	US-09-341-587-7
8	46.2	1.5	21721	4	US-09-269-939A-41
9	45.6	1.5	191	4	US-09-621-976-9448
10	44.8	1.5	23187	4	US-09-499-522-1
11	43.8	1.5	300	3	US-09-157-177-118
12	43.8	1.5	6063	1	US-08-195-744-4
13	43.2	1.4	819	4	US-08-788-278-4
14	43.2	1.4	819	4	US-09-369-247-44
15	43.2	1.4	941	4	US-09-205-258-13
16	43.2	1.4	941	4	US-09-205-258-218
17	43.2	1.4	3634	3	US-09-166-186-1
18	43.2	1.4	3634	3	US-09-313-932-1
19	43.2	1.4	3634	3	US-09-109-663-34
20	43.2	1.4	392000	4	US-10-027-983-11
21	43	1.4	2426	4	US-10-011-858-1
22	42.8	1.4	38653	4	US-09-922-445-1
23	42.2	1.4	161652	4	US-09-497-855A-40
24	41.6	1.4	246240	2	US-08-724-394A-20
25	41.6	1.4	246240	2	US-08-724-394A-21
26	41.6	1.4	246240	2	US-08-724-394A-22
27	41.4	1.4	78	3	US-09-030-156-20

Sequence 20, Appl
Sequence 23, Appl
Sequence 33, Appl
Sequence 1, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 928, Appl
Sequence 1379, Ap
Sequence 19, Appl
Sequence 19, Appl
Sequence 15457, A
Sequence 8, Appl
Sequence 156, App
Sequence 59, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 2813, Ap
Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Hardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PTZgpt-Fls
US-08-232-463-14

Query Match

2.7%; Score 81.8; DB 1; Length 7218;

[illegible]

RESULT 2
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 INMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

; LENGTH: 7218 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; CLONE: pTZ9pt-Fls
 US-08-232-463-14

Query Match 2.4%; Score 70.8; DB 1; Length 7218;
 Best Local Similarity 9.5%; Pred. No. 1.8e-10;
 Matches 45; Conservative 237; Mismatches 194; Indels 0; Gaps 0;

Qy	1003	AGTGAAGACAGAGCTCTGTATCTCCCTCAGTGGCTTCACAAATGCCCTGGCATATAGTAGTT	1062		1003	AGTGAAGACAGAGCTCTGTATCTCCCTCAGTGGCTTCACAAATGCCCTGGCATATAGTAGTT
Db	1513	AGTTTCAAAAACCGCATGTAGGCATCCTGTAAATTACCTACTATGACAGTAGTTAAAG	1454		1513	AGTTTCAAAAACCGCATGTAGGCATCCTGTAAATTACCTACTATGACAGTAGTTAAAG
Qy	1063	ATTTCAGTGCAGTGTTCCTTGGATGCAATGAATGAATAAATAAATGAAGAAATGAATGA	1122		1063	ATTTCAGTGCAGTGTTCCTTGGATGCAATGAATGAATGAATAAATAAATGAAGAAATGAATGA
Db	1453	AGATAGAAGAAATTGGTACRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNR	1394		1453	AGATAGAAGAAATTGGTACRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNR
Qy	1123	AGAAATAACGATGGGTGATTGCAGATGACAGATGACAGTTGTGGATATGTTGTCAACACTGAT	1182		1123	AGAAATAACGATGGGTGATTGCAGATGACAGATGACAGTTGTGGATATGTTGTCAACACTGAT
Db	1393	RRNR	1334		1393	RRNR
Qy	1183	AGTGTTCACAGATAAATGTGCCACAGCAGATCTCTGGGTACAGACTAGAGCATGTGTGTT	1242		1183	AGTGTTCACAGATAAATGTGCCACAGCAGATCTCTGGGTACAGACTAGAGCATGTGTGTT
Db	1333	RRNR	1274		1333	RRNR
Qy	1243	ATAGTAAATAGTACTGGATTGCAAACTGACAGATGTGTAATGTGCAAAAGCAGCAGCAC	1302		1243	ATAGTAAATAGTACTGGATTGCAAACTGACAGATGTGTAATGTGCAAAAGCAGCAGCAC
Db	1273	RRNR	1214		1273	RRNR
Qy	1303	ATTGTGTCACAGATGCACTGAGAAATGTGTAGGGCCACAGAAAGGATATCGTATAAGCAC	1362		1303	ATTGTGTCACAGATGCACTGAGAAATGTGTAGGGCCACAGAAAGGATATCGTATAAGCAC
Db	1213	RRNR	1154		1213	RRNR
Qy	1363	AGTAGATAAAATAATGTCTTAAATGACAGCTGGCAGTATCTGGGGATGACAGCTCAAAA	1422		1363	AGTAGATAAAATAATGTCTTAAATGACAGCTGGCAGTATCTGGGGATGACAGCTCAAAA
Db	1153	RRNR	1094		1153	RRNR
Qy	1423	GACAGTACTTTTCAATGCAGGGGACAAAGTCTGGGTATACCCCTCTGAAAAGAAG	1478		1423	GACAGTACTTTTCAATGCAGGGGACAAAGTCTGGGTATACCCCTCTGAAAAGAAG
Db	1093	RRNR	1038		1093	RRNR

RESULT 3
 US-09-205-258-182
 ; Sequence 182; Application US/09205258
 ; Patent No. 6525174
 ; GENERAL INFORMATION:
 ; APPLICANT: Young et al.
 ; TITLE OF INVENTION: 207 Human Secreted Proteins
 ; FILE REFERENCE: P2007P1
 ; CURRENT APPLICATION NUMBER: US/09/205,258
 ; CURRENT FILING DATE: 1998-12-04
 ; EARLIER APPLICATION NUMBER: PCT/US98/11422
 ; EARLIER FILING DATE: 1998-06-04
 ; EARLIER APPLICATION NUMBER: 60/048,885
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/049,375
 ; EARLIER FILING DATE: 1997-06-05
 ; EARLIER APPLICATION NUMBER: 60/048,881
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,880
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,896
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/049,020
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,876
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,895
 ; EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,952
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,953
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 182
LENGTH: 1128
TYPE: DNA
ORGANISM: Homo sapiens
US-09-205-258-182

Query Match 1.9%; Score 58.4; DB 4; Length 1128;
Best Local Similarity 74.0%; Pred. No. 3.1e-07;
Matches 74; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1017 TCTTCTTATCTCAGTGCCTCTCACAATGCTGGCATATAGTAGTATTTCAGTACTGTT 1076
DB 905 TCTTCTTATCTCAGTGCCTCTCACAATGCTGGCATATAGTAGTATTTCAGTACTGTT 964
QY 1077 TCTTGGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1116
DB 965 TCTTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1004

RESULT 4
US-09-489-847-58
Sequence 58, Application US/09489847
Patent No. 6476195
GENERAL INFORMATION:
APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCES: P2031PI
CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/096,319
EARLIER FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58
LENGTH: 619
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (526)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (619)
OTHER INFORMATION: n equals a,t,g, or c
US-09-489-847-58

Query Match 1.6%; Score 48.8; DB 4; Length 619;
Best Local Similarity 63.2%; Pred. No. 0.00017;
Matches 74; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
QY 1014 GAGTCTTCTTATCTCAGTGCCTCTCACAATGCTGGCATATAGTAGTATTTCAGTACTGTT 1073
DB 498 GAAATTTTGTATTACAGTGCCTCTTGTCTGCGCCTAGAACGCTCAATTAAT 557
QY 1074 GTTCTTCGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1130
DB 558 GTTCTTCGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 614

RESULT 5
US-09-269-939A-19
Sequence 19, Application US/09269939A
Patent No. 635431
GENERAL INFORMATION:
APPLICANT: Bihaun, Bernard
APPLICANT: Bougueret, Lydie
APPLICANT: Yen-Potin, Frances
TITLE OF INVENTION: LSR Receptor, Its Activity, Its Cloning and Its Application To
TITLE OF INVENTION: The Diagnosis Prevention And/or Treatment of Obesity and
TITLE OF INVENTION: Related Risks or Complications
FILE REFERENCE: GENSET.035APC

CURRENT APPLICATION NUMBER: US/09/269,939A
CURRENT FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: FR 97/10068
PRIOR FILING DATE: 1997-08-06
PRIOR APPLICATION NUMBER: FR 98/05032
PRIOR FILING DATE: 1998-04-22
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patent.pm
SEQ ID NO 19
LENGTH: 22976
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 1898..2253
NAME/KEY: exon
LOCATION: 3437..3781
NAME/KEY: exon
LOCATION: 12065..12184
NAME/KEY: exon
LOCATION: 15045..15101
NAME/KEY: exon
LOCATION: 15666..15812
NAME/KEY: exon
LOCATION: 19479..19652
NAME/KEY: exon
LOCATION: 19739..19858
NAME/KEY: exon
LOCATION: 19956..20087
NAME/KEY: exon
LOCATION: 20223..20854
NAME/KEY: exon
LOCATION: 20944..21094
NAME/KEY: Misc Feature
LOCATION: 19956..19958
OTHER INFORMATION: Potential variant splicing site AAG
US-09-269-939A-19

Query Match 1.6%; Score 48; DB 4; Length 22976;
Best Local Similarity 68.6%; Pred. No. 0.0036;
Matches 81; Conservative 0; Mismatches 35; Indels 2; Gaps 1;
QY 1020 TGTATCTCAGTGGCTCTCAGCAATGCTGCGCATATAGTAGTATTTCAGTACTGT--TT 1077
DB 9755 TGGTATCCAGGTGCTCTCAATATCTGCTAGAACATAGGTGGTACTCAGTAATATTGTT 9814
QY 1078 CTTCGATGAATCAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1135
DB 9815 GAAGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGTC 9872

RESULT 6
US-09-146-053-5
Sequence 5, Application US/09146053A
Patent No. 6399349
GENERAL INFORMATION:
APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Venema, Richard C.
TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MCG103
CURRENT APPLICATION NUMBER: US/09/146,053A
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,854
EARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 44453
TYPE: DNA
ORGANISM: Homo sapiens
US-09-146-053-5

Query Match 1.6%; Score 47.6; DB 4; Length 44453;
Best Local Similarity 59.7%; Pred. No. 0.0074;
Matches 80; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
QY 1023 TATCTCAGTGGCTCTCAGCAATGCTGCGCATATAGTAGTATTTCAGTACTGTTCCTGG 1082
DB 30421 TACCCCTAGGACCTAGCAAGTGTCTGGCATATAGCAGCGCCAGCAAGTGTTCATGA 30480
QY 1083 ATCAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1142
DB 30481 ATCAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 30540
QY 1143 TCCAGGATGAACAG 1156
DB 30541 TGTCAATAACAG 30554
RESULT 7
US-09-341-587-7
Sequence 7, Application US/09341587
Patent No. 6346606
GENERAL INFORMATION:
APPLICANT: Mollenhauer, Jan
TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REFERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 28720
TYPE: DNA
ORGANISM: Homo sapiens
US-09-341-587-7

Query Match 1.6%; Score 47; DB 4; Length 28720;
Best Local Similarity 57.5%; Pred. No. 0.0084;
Matches 103; Conservative 0; Mismatches 75; Indels 1; Gaps 1;
QY 974 TTTCTGCTTTTGTACAGTGAACCTTCCTGAAGTGAAGCAAGAGTCT-TGTTATCTCAGT 1032
DB 12051 TATCTTTCTGCCAACTGCAATTCCTGAAGCGGCGGCCATGTCTGCCCTTTTCATAAT 12110
QY 1033 GCTCTCAATGCTGCGCATATAGTAGTATTTCAGTCACTGTTTCTTGGATGAATGAAT 1092
DB 12111 GTATCTTATTATCTAGCAATGTCTGCTGCTTTCAAGACTGTTTATTGAAGGAATAAT 12170
QY 1093 GAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATG 1151
DB 12171 GAGTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATG 12229

RESULT 8
US-09-269-939A-41
Sequence 41, Application US/09269939A
Patent No. 6633431
GENERAL INFORMATION:
APPLICANT: Bihain, Bernard
APPLICANT: Bougueleret, Lydie
APPLICANT: Yen-Potin, Françoise
TITLE OF INVENTION: LSR Receptor, Its Activity, Its Cloning and Its Application To
Prevention And/or Treatment of Obesity and
Title of Invention: Related Risks or Complications
FILE REFERENCE: GENSET.035APC
CURRENT APPLICATION NUMBER: US/09/269,939A
CURRENT FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: FR 97/10088
PRIOR FILING DATE: 1997-08-06
PRIOR APPLICATION NUMBER: FR 98/05032
PRIOR FILING DATE: 1998-04-22
NUMBER OF SEQ ID NOS: 41

[illegible]

```
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9448
; LENGTH: 191
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-9448

Query Match      1.5%; Score 45.6; DB 4; Length 191;
Best Local Similarity 68.5%; Pred. No. 0.00074;
Matches 63; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1039 CACAATGCTGCGATATAGTATTTCAGTCACTCTTCTTGGATGAATGAATGAATGA 1098
DB 88 CCTGTCTCTGCACATAGTACGCACTCAATAATTCATTAAAGGAATGAATGAATGA 147
QY 1099 ATAATAAATGAAGAAATCAATGACAAATAA 1130
DB 148 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 179

RESULT 10
US-09-499-522-1
; Sequence 1, Application US/09499522
; Patent No. 6479238
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: POLYMORPHIC MARKERS OF THE LSR GENE
; FILE REFERENCE: GENSET.053AUS
; CURRENT APPLICATION NUMBER: US/09/499,522
; CURRENT FILING DATE: 2000-02-10
; EARLIER APPLICATION NUMBER: US 60/119,592
; EARLIER FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: US 60/144,784
; EARLIER FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 23187
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2001..2356
; OTHER INFORMATION: exon1
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3540..3884
; OTHER INFORMATION: exon2
; FEATURE:
; NAME/KEY: exon
; LOCATION: 12163..12282
; OTHER INFORMATION: exon3
; FEATURE:
; NAME/KEY: exon
; LOCATION: 15144..15200
; OTHER INFORMATION: exon4
; FEATURE:
; NAME/KEY: exon
; LOCATION: 15765..15911
; OTHER INFORMATION: exon5
; FEATURE:

; NAME/KEY: exon
; LOCATION: 19579..19752
; OTHER INFORMATION: exon6
; FEATURE:
; NAME/KEY: exon
; LOCATION: 19899..19958
; OTHER INFORMATION: exon7
; FEATURE:
; NAME/KEY: exon
; LOCATION: 20056..20187
; OTHER INFORMATION: exon8
; FEATURE:
; NAME/KEY: exon
; LOCATION: 20329..20957
; OTHER INFORMATION: exon9
; FEATURE:
; NAME/KEY: exon
; LOCATION: 21047..21187
; OTHER INFORMATION: exon10
; FEATURE:
; NAME/KEY: polyA signal
; LOCATION: 21168..21173
; OTHER INFORMATION: AATAAA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..2000
; OTHER INFORMATION: potential 5'regulatory region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 22324..23187
; OTHER INFORMATION: homology with USP2 gene in ref: embl Y07661
; NAME/KEY: primer_bind
; LOCATION: 523..544
; OTHER INFORMATION: upstream amplification primer 17-2
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1047..1068
; OTHER INFORMATION: downstream amplification primer 17-2, complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 946..963
; OTHER INFORMATION: upstream amplification primer 99-4576
; NAME/KEY: primer_bind
; LOCATION: 1385..1402
; OTHER INFORMATION: downstream amplification primer 99-4576, complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1096..1115
; OTHER INFORMATION: upstream amplification primer 9-19
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1616..1635
; OTHER INFORMATION: downstream amplification primer 9-19, complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1602..1621
; OTHER INFORMATION: upstream amplification primer 9-20
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 2074..2093
; OTHER INFORMATION: downstream amplification primer 9-20, complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 2036..2053
; OTHER INFORMATION: upstream amplification primer 99-4557
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 2563..2580
; OTHER INFORMATION: downstream amplification primer 99-4557, complement
; FEATURE:
; NAME/KEY: primer_bind
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LOCATION: 2084..2102
OTHER INFORMATION: upstream amplification primer 9-1
FEATURE:
NAME/KEY: primer bind
LOCATION: 2483..2500
OTHER INFORMATION: downstream amplification primer 9-1, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 2470..2489
OTHER INFORMATION: upstream amplification primer 9-21, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 2062..2081
OTHER INFORMATION: downstream amplification primer 9-21
FEATURE:
NAME/KEY: primer bind
LOCATION: 3455..3474
OTHER INFORMATION: upstream amplification primer 9-3
FEATURE:
NAME/KEY: primer bind
LOCATION: 3882..3901
OTHER INFORMATION: downstream amplification primer 9-3, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 3775..3792
OTHER INFORMATION: upstream amplification primer 99-4558
FEATURE:
NAME/KEY: primer bind
LOCATION: 4336..4356
OTHER INFORMATION: downstream amplification primer 99-4558, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 4902..4920
OTHER INFORMATION: upstream amplification primer 99-14419, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 4444..4463
OTHER INFORMATION: downstream amplification primer 99-14419
FEATURE:
NAME/KEY: primer bind
LOCATION: 6638..6655
OTHER INFORMATION: upstream amplification primer 99-4577
FEATURE:
NAME/KEY: primer bind
LOCATION: 7072..7089
OTHER INFORMATION: downstream amplification primer 99-4577, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 7995..8012
OTHER INFORMATION: upstream amplification primer 99-4559
FEATURE:
NAME/KEY: primer bind
LOCATION: 8576..8593
OTHER INFORMATION: downstream amplification primer 99-4559, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 9622..9639
OTHER INFORMATION: upstream amplification primer 99-3148
FEATURE:
NAME/KEY: primer bind
LOCATION: 10023..10040
OTHER INFORMATION: downstream amplification primer 99-3148, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 9964..9981
OTHER INFORMATION: upstream amplification primer 99-4560
FEATURE:
NAME/KEY: primer bind
LOCATION: 10546..10563
OTHER INFORMATION: downstream amplification primer 99-4560, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 10996..11015

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; OTHER INFORMATION: upstream amplification primer 99-14411 , complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 10492..10512
; OTHER INFORMATION: downstream amplification primer 99-14411
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 11972..11990
; OTHER INFORMATION: upstream amplification primer 99-4561
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 12481..12501
; OTHER INFORMATION: downstream amplification primer 99-4561 , complement

Query Match      1.5%; Score 44.8; DB 4; Length 23187;
Best Local Similarity 71.6%; Pred. No. 0.034;
Matches 73; Conservative 0; Mismatches 27; Indels 2; Gaps 1;

Qy 1020 TGTATTCTCAGTGCCTCTCACAAATGCTGGGCATATAGTAGTTATTTCAGTGACTGT--TT 1077
Db 9860 TGGTATCCCGAGGTCTCAAAATCTGCCTAGAACATAGGTGGTACTCAGTAATATTGTT 9919

Qy 1078 CTTGGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1119
Db 9920 GAAGGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 9961

RESULT 11
US-09-157-177-118
; Sequence 118, Application US/09157177
; Patent No. 6090558
; GENERAL INFORMATION:
; APPLICANT: Butler, John M.
; APPLICANT: Li, Jia
; APPLICANT: Monforte, Joseph A.
; APPLICANT: Becker, Christopher H.
; TITLE OF INVENTION: DNA TYPING BY MASS SPECTROMETRY WITH POLYMORPHIC DNA
; TITLE OF INVENTION: REPEAT MARKERS
; FILE REFERENCE: GETR:017/GSTRO17P
; CURRENT APPLICATION NUMBER: US/09/157,177
; CURRENT FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: 60/059,415
; EARLIER FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 118
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-157-177-118

Query Match      1.5%; Score 43.8; DB 3; Length 300;
Best Local Similarity 72.2%; Pred. No. 0.0036;
Matches 57; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 1045 GCTGGCATATAGTATTATTCAGTGACTGTTCTTGGATGAATGAATGAATGAATGAATGAAT 1104
Db 17 GACTGGCAGCAGACACAGGCACCTTAGGGAAACCTCCTCAGTAATGAATGAATGAATGAATGAAT 76

Qy 1105 AAATGAAGAAATGAATGAA 1123
Db 77 GAATGAATGAATGAATGAA 95

RESULT 12
US-08-195-744-4
; Sequence 4, Application US/08195744
; Patent No. 5639607
; GENERAL INFORMATION:
; APPLICANT: DESNICK, R.
; APPLICANT: WETMUR, J.
; TITLE OF INVENTION: METHODS FOR DETERMINING SUSCEPTIBILITY
; TITLE OF INVENTION: TO LEAD POISONING

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Query Match      1.4%; Score 43.2; DB 4; Length 819;  
Best Local Similarity   65.6%; Pctid.No.0.011;  
Matches    63; Conservative     0; Mismatches    33; Indels       0; Gaps         0;
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QY 1025 TCCTCAGTGGCTTCACAAATGCCGTGGCATATTAGTAGTTATTTCAAGTGACTGTTCTTCGCAT 1084
|||
Db 252 TCCTCAGCATCTATCGCAGGGCCCTGGCACATAAAGGCANCAAATAAATGTTTGTTCAT 193

QY 1085 GAATGAATGAATCAATAAATAAMTAAGAAGAAAATGAAT 1120
|||||
Db 192 AAATGAATGAATGAGTGAATGAGCCAACAACAACT 157

RESULT 15
US-09-205-258-13/c
; Sequence 13, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: FZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06